

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 17:59:08 ; Search time 596 Seconds
(without alignments)
9967.860 Million cell updates/sec

Title: US-10-063-736-129
Perfect score: 1177
Sequence: 1 aacttctacatggcctcct.....ataaccacacatggcaaaaa 1177

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 3327077 seqs, 2523723180 residues

Total number of hits satisfying chosen parameters: 6654154

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications NA:*

- 1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:*
- 2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:*
- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq:*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq:*
- 5: /cgn2_6/ptodata/1/pubpna/US07_NEW_PUB.seq:*
- 6: /cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
- 7: /cgn2_6/ptodata/1/pubpna/US08_NEW_PUB.seq:*
- 8: /cgn2_6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
- 9: /cgn2_6/ptodata/1/pubpna/US09A_PUBCOMB.seq:*
- 10: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:*
- 11: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:*
- 12: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq:*
- 13: /cgn2_6/ptodata/1/pubpna/US09_NEW_PUB.seq2:*
- 14: /cgn2_6/ptodata/1/pubpna/US10A_PUBCOMB.seq:*
- 15: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:*
- 16: /cgn2_6/ptodata/1/pubpna/US10C_PUBCOMB.seq:*
- 17: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq:*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1177	100.0	1177	13	US-10-206-915-381 Sequence 381, App
2	1177	100.0	1177	13	US-10-199-670-381 Sequence 381, App
3	1177	100.0	1177	13	US-10-201-858-381 Sequence 381, App
4	1177	100.0	1177	13	US-10-081-056-271 Sequence 271, App
5	1177	100.0	1177	13	US-10-219-535-211 Sequence 211, App
6	1177	100.0	1177	13	US-10-232-230-211 Sequence 211, App
7	1177	100.0	1177	13	US-10-205-890-381 Sequence 381, App
8	1177	100.0	1177	13	US-10-208-024-381 Sequence 381, App
9	1177	100.0	1177	13	US-10-201-853-381 Sequence 381, App
10	1177	100.0	1177	13	US-10-063-745-129 Sequence 129, App
11	1177	100.0	1177	13	US-10-063-512-129 Sequence 129, App
12	1177	100.0	1177	13	US-10-063-513-129 Sequence 129, App
13	1177	100.0	1177	13	US-10-063-569-129 Sequence 129, App
14	1177	100.0	1177	13	US-10-063-551-129 Sequence 129, App

15	1177	100.0	1177	13	US-10-174-581-381	Sequence 381, App
16	1177	100.0	1177	13	US-10-176-483-381	Sequence 381, App
17	1177	100.0	1177	13	US-10-176-749-381	Sequence 381, App
18	1177	100.0	1177	13	US-10-176-914-381	Sequence 381, App
19	1177	100.0	1177	13	US-10-176-915-381	Sequence 381, App
20	1177	100.0	1177	13	US-10-063-555-129	Sequence 129, App
21	1177	100.0	1177	13	US-10-063-563-129	Sequence 129, App
22	1177	100.0	1177	13	US-10-063-594-129	Sequence 129, App
23	1177	100.0	1177	13	US-10-063-553-129	Sequence 129, App
24	1177	100.0	1177	13	US-10-063-554-129	Sequence 129, App
25	1177	100.0	1177	13	US-10-176-484-381	Sequence 381, App
26	1177	100.0	1177	13	US-10-180-550-381	Sequence 381, App
27	1177	100.0	1177	13	US-10-183-014-381	Sequence 381, App
28	1177	100.0	1177	13	US-10-187-738-381	Sequence 381, App
29	1177	100.0	1177	13	US-10-187-740-381	Sequence 381, App
30	1177	100.0	1177	13	US-10-187-883-381	Sequence 381, App
31	1177	100.0	1177	13	US-10-194-363-381	Sequence 381, App
32	1177	100.0	1177	13	US-10-194-460-381	Sequence 381, App
33	1177	100.0	1177	13	US-10-194-463-381	Sequence 381, App
34	1177	100.0	1177	13	US-10-194-484-381	Sequence 381, App
35	1177	100.0	1177	13	US-10-195-884-381	Sequence 381, App
36	1177	100.0	1177	13	US-10-195-896-381	Sequence 381, App
37	1177	100.0	1177	13	US-10-196-744-381	Sequence 381, App
38	1177	100.0	1177	13	US-10-196-755-381	Sequence 381, App
39	1177	100.0	1177	13	US-10-196-757-381	Sequence 381, App
40	1177	100.0	1177	13	US-10-197-704-381	Sequence 381, App
41	1177	100.0	1177	13	US-10-197-710-381	Sequence 381, App
42	1177	100.0	1177	13	US-10-198-758-381	Sequence 381, App
43	1177	100.0	1177	13	US-10-198-766-381	Sequence 381, App
44	1177	100.0	1177	13	US-10-199-304-381	Sequence 381, App
45	1177	100.0	1177	13	US-10-199-309-381	Sequence 381, App

ALIGNMENTS

RESULT 1

US-10-206-915-381
; Sequence 381, Application US/10206915
; Publication No. US20040029221A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C513
; CURRENT APPLICATION NUMBER: US/10/206,915
; CURRENT FILING DATE: 2002-07-26
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28


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; PRIOR FILING DATE: 2001-03-01
; PRIOR APPLICATION NUMBER: US 09/802,706
; PRIOR FILING DATE: 2001-03-09
; PRIOR APPLICATION NUMBER: US 09/808,689
; PRIOR FILING DATE: 2001-03-14
; PRIOR APPLICATION NUMBER: US 09/816,744
; PRIOR FILING DATE: 2001-03-22
; PRIOR APPLICATION NUMBER: US 09/828,366
; PRIOR FILING DATE: 2001-04-05
; PRIOR APPLICATION NUMBER: US 09/854,208
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/854,280
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: US 09/866,028
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/866,034
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: PCT/US01/17092
; PRIOR FILING DATE: 2001-05-25
; PRIOR APPLICATION NUMBER: US 09/870,574
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17443
; PRIOR FILING DATE: 2001-05-30
; PRIOR APPLICATION NUMBER: PCT/US01/17800
; PRIOR FILING DATE: 2001-06-01
; PRIOR APPLICATION NUMBER: PCT/US01/19692
; PRIOR FILING DATE: 2001-06-20
; PRIOR APPLICATION NUMBER: PCT/US01/00000
; PRIOR FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 383
; SEQ ID NO 271
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homosapiens
US-10-081-056-271

Query Match      100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy      1  AACTTCTACATGGGCCTCTGCTGGTCTCTTCCTCAGCCTCCTGCCGGTGGCCTAC 60
Db      1  AACTTCTACATGGGCCTCTGCTGGTCTCTTCCTCAGCCTCCTGCCGGTGGCCTAC 60

Qy     61  ACCATCATGTCCCTCCACCTCTTGTACTGCGGGCGGTTTCAGGTGCAGAGTCTCAGTT 120
Db     61  ACCATCATGTCCCTCCACCTCTTGTACTGCGGGCGGTTTCAGGTGCAGAGTCTCAGTT 120

Qy    121  GCCGGGAGCACCTCCCTCCGAGGCAGTCTGTCTCAGAGGGCCTCGGCCCAGAATTCCA 180
Db    121  GCCGGGAGCACCTCCCTCCGAGGCAGTCTGTCTCAGAGGGCCTCGGCCCAGAATTCCA 180

Qy    181  GTTCTGGTTTCATGCCAGCCTGTAAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCA 240
Db    181  GTTCTGGTTTCATGCCAGCCTGTAAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCA 240

Qy    241  TTTAAGAGGGTTTTCTGCGCAGGATGGAATGTTAGGTGCTTCTGTCTGCGTGTTCAT 300
Db    241  TTTAAGAGGGTTTTCTGCGCAGGATGGAATGTTAGGTGCTTCTGTCTGCGTGTTCAT 300

Qy    301  TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGTCTTGAATGAGGAACCTGAGAAAAATT 360
Db    301  TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGTCTTGAATGAGGAACCTGAGAAAAATT 360

Qy    361  AATTTCTCATGTATTTTCTCATTTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Db    361  AATTTCTCATGTATTTTCTCATTTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420

Qy    421  GGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCAAATCAGGGTAAC 480
Db    421  GGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCAAATCAGGGTAAC 480

Qy    481  TGGGATATCCATCACATCAAAACATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 540
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Db      481  TGGGATATCCATCACATCAAAACATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 540
Qy     541  TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT 600
Db     541  TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT 600
Qy     601  TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAAT 660
Db     601  TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAAT 660
Qy     661  GCCCAACTAATTTTGTATTTTATTTAGTAGAGACGGGGTTTTTGGCATGTTGCCAGGCTGGC 720
Db     661  GCCCAACTAATTTTGTATTTTATTTAGTAGAGACGGGGTTTTTGGCATGTTGCCAGGCTGGC 720
Qy     721  CTTGAACTCCTGGCCTCAAAACAATCCACTTGCCTCGGCCCTCCCAAAGTGTATGATTACA 780
Db     721  CTTGAACTCCTGGCCTCAAAACAATCCACTTGCCTCGGCCCTCCCAAAGTGTATGATTACA 780
Qy     781  GCGGTGAGCCACCGTGCCTGGCCTAAACAATTTATCTTTTCTTTGTGTTGGGAACCTTTGAA 840
Db     781  GCGGTGAGCCACCGTGCCTGGCCTAAACAATTTATCTTTTCTTTGTGTTGGGAACCTTTGAA 840
Qy     841  ATTATACAATGAATTTATCTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Db     841  ATTATACAATGAATTTATCTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Qy     901  TCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAAACCAACCGTACTTTCATCCCACTC 960
Db     901  TCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAAACCAACCGTACTTTCATCCCACTC 960
Qy     961  CTCTCTATCCTTCCCAACCTCTGTATCACCCTCATCTTCTACTCTCTACCTCCATGAGATCCAC 1020
Db     961  CTCTCTATCCTTCCCAACCTCTGTATCACCCTCATCTTCTACTCTCTACCTCCATGAGATCCAC 1020
Qy    1021  TTTTGTAGCTCCCAACATGTGAGTAAGAAAATGCAATATTTTCTTCTGTGCTGCTGCTTA 1080
Db    1021  TTTTGTAGCTCCCAACATGTGAGTAAGAAAATGCAATATTTTCTTCTGTGCTGCTGCTTA 1080
Qy    1081  TTTCACTTAACATAATGACTTCTCTGTTCCCATCCATGTTGCTGCAAAATGACAGGATTTTCT 1140
Db    1081  TTTCACTTAACATAATGACTTCTCTGTTCCCATCCATGTTGCTGCAAAATGACAGGATTTCT 1140
Qy    1141  TCTTAATTTCAATTTAAATAAACACACATGGCAAAA 1177
Db    1141  TCTTAATTTCAATTTAAATAAACACACATGGCAAAA 1177
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RESULT 5
US-10-219-535-211
; Sequence 211, Application US/10219535
; Publication No. US20040044179A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3530P1C60
; CURRENT APPLICATION NUMBER: US/10/219,535
; CURRENT FILING DATE: 2002-08-14
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
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; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25
; PRIOR APPLICATION NUMBER: 60/079656
; PRIOR FILING DATE: 1998-03-26
; PRIOR APPLICATION NUMBER: 60/079728
; PRIOR FILING DATE: 1998-03-27
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 246
; SEQ ID NO 211
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-219-535-211

Query Match      100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCTACATGGGCTCCTGCTGCTGGTCTCTTCCCTCAGCCTCCTGCGGTGGCTTAC 60
Db 1 AACTTCTACATGGGCTCCTGCTGCTGGTCTCTTCCCTCAGCCTCCTGCGGTGGCTTAC 60
QY 61 ACCATCATGTCCTCCACCCCTCCTTTGACTGCGGGCCGTTGAGTGCAGAGTCTCAGTT 120
Db 61 ACCATCATGTCCTCCACCCCTCCTTTGACTGCGGGCCGTTGAGTGCAGAGTCTCAGTT 120
QY 121 GCGCGGAGACACCTCCCTCCCGAGGAGCTGCTGCTCAGAGGCTCGGCCAGCAATTTCCA 180
Db 121 GCGCGGAGACACCTCCCTCCCGAGGAGCTGCTGCTCAGAGGCTCGGCCAGCAATTTCCA 180
QY 181 GTTCTGTTTCATGCCAGCCTGTAAGAGGCCATGGAACTTTGGGTGAATCACCGATGCCA 240
Db 181 GTTCTGTTTCATGCCAGCCTGTAAGAGGCCATGGAACTTTGGGTGAATCACCGATGCCA 240
QY 241 TTTAAGAGGTTTCTGCCAGGATGGAATGTTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db 241 TTTAAGAGGTTTCTGCCAGGATGGAATGTTAGTCTGCTGCTGCTGCTGCTGCTGCTGCT 300
QY 301 TTCAGTAGCCACAGCCACCTGTGGCCGTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
Db 301 TTCAGTAGCCACAGCCACCTGTGGCCGTTGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360
QY 361 AATTCTCATGTATTTTCTCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 420
Db 361 AATTCTCATGTATTTTCTCATTTATTTATTTATTTATTTATTTATTTATTTATTTATTTATTT 420
QY 421 GGGGTACATGTATTTGGATACATGTATACATATATAATATGATCAATCAGGGTAAC 480
Db 421 GGGGTACATGTATTTGGATACATGTATACATATATAATATGATCAATCAGGGTAAC 480
QY 481 TGGGATATCCATCACATCAAACTTTATTTTATTTATTTTATTTATTTATTTATTTATTTATTTATTT 540
Db 481 TGGGATATCCATCACATCAAACTTTATTTTATTTATTTTATTTATTTATTTATTTATTTATTTATTT 540
QY 541 TCACCCAGGCTGGAGTGCAGTGGTGGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGT 600
Db 541 TCACCCAGGCTGGAGTGCAGTGGTGGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGT 600
QY 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGTGGGACTACAGGCAATGACCAACAAT 660
Db 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGTGGGACTACAGGCAATGACCAACAAT 660
QY 661 GCCCAACTAATTTTGTATTTTATTTAGTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGC 720

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Db 661 GCCCAACTAATTTTGTATTTTATTTAGTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGC 720
QY 721 CTTGAACCTCCTGGCCTCAAAACAATCCACTTGCCTCGGCCCTCCCAAAGTGTATGATTACA 780
Db 721 CTTGAACCTCCTGGCCTCAAAACAATCCACTTGCCTCGGCCCTCCCAAAGTGTATGATTACA 780
QY 781 GCGGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTGTGTTGGGAACCTTTGAA 840
Db 781 GCGGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTGTGTTGGGAACCTTTGAA 840
QY 841 ATTATACATGAATTTATTTGTTAACTGTCATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
Db 841 ATTATACATGAATTTATTTGTTAACTGTCATCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 900
QY 901 TCTTCCCTCTATCTAACTGTATATTGTACCAAGTTAACCACCGTACTTTCATCCCCACTC 960
Db 901 TCTTCCCTCTATCTAACTGTATATTGTACCAAGTTAACCACCGTACTTTCATCCCCACTC 960
QY 961 CTCTCTATCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACTCTCTACTCTCTACTCTCTACT 1020
Db 961 CTCTCTATCTTCCCAACCTCTGATCACCTCATTCTACTCTCTACTCTCTACTCTCTACTCTCTACT 1020
QY 1021 TTTTGTAGCTCCACATGTGAGTAAGAAAAATGCAATATTTGCTTTCTGTGCTGGCTTA 1080
Db 1021 TTTTGTAGCTCCACATGTGAGTAAGAAAAATGCAATATTTGCTTTCTGTGCTGGCTTA 1080
QY 1081 TTTCACTTAACATAATGACTTCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTCGT 1140
Db 1081 TTTCACTTAACATAATGACTTCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTCGT 1140
QY 1141 TCTTAATTTCAATTAATAAACACACATGGCAAAAA 1177
Db 1141 TCTTAATTTCAATTAATAAACACACATGGCAAAAA 1177

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RESULT 6

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US-10-232-230-211
; Sequence 211, Application US/10232230
; Publication No. US2004004180A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Desnoyers, Luc
; APPLICANT: Gerritsen, Mary
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, J. Christopher
; APPLICANT: Gurney, Austin L.
; APPLICANT: Smith, Victoria
; APPLICANT: Stephan, Jean-Philippe F.
; APPLICANT: Watanabe, Colin L.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3530P1C103
; CURRENT APPLICATION NUMBER: US/10/232,230
; PRIOR FILING DATE: 2002-08-29
; PRIOR APPLICATION NUMBER: 10/119,480
; PRIOR FILING DATE: 2002-04-09
; PRIOR APPLICATION NUMBER: 60/059113
; PRIOR FILING DATE: 1997-09-17
; PRIOR APPLICATION NUMBER: 60/062287
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063549
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/064103
; PRIOR FILING DATE: 1997-10-31
; PRIOR APPLICATION NUMBER: 60/069873
; PRIOR FILING DATE: 1997-12-17
; PRIOR APPLICATION NUMBER: 60/078910
; PRIOR FILING DATE: 1998-03-20
; PRIOR APPLICATION NUMBER: 60/079294
; PRIOR FILING DATE: 1998-03-25

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Query Match      100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCTACATGGGCTCCTGCTGCTGGTCTCTTCCCTCAGCCTCCTGCCGGTGGCTTAC 60
Db 1 AACTTCTACATGGGCTCCTGCTGCTGGTCTCTTCCCTCAGCCTCCTGCCGGTGGCTTAC 60

QY 61 ACCATCATGTCCCTCCCACCCCTCCCTTTGACTGCGGGCCGTTACAGGTGCAGAGTCTCAGTT 120
Db 61 ACCATCATGTCCCTCCCACCCCTCCCTTTGACTGCGGGCCGTTACAGGTGCAGAGTCTCAGTT 120

QY 121 GCCCGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCTCGGCCCCAGAAATCCA 180
Db 121 GCCCGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCTCGGCCCCAGAAATCCA 180

QY 181 GTTCTGTTTCATGCCAGCCTGTAAAGGCCCATGGAACCTTTGGGTGAATCACCCGATGCCA 240
Db 181 GTTCTGTTTCATGCCAGCCTGTAAAGGCCCATGGAACCTTTGGGTGAATCACCCGATGCCA 240

QY 241 TTTAAGAGGTTTCTGCCAGGATGGAAGTTAGTCTGTTCTGTCTGCGCTGTTTCAT 300
Db 241 TTTAAGAGGTTTCTGCCAGGATGGAAGTTAGTCTGTTCTGTCTGCGCTGTTTCAT 300

QY 301 TTCAGTAGCCACGACCCCTGTGGCGGTGAGTGTCTTGAATGAGGAACCTGAGAAAATT 360
Db 301 TTCAGTAGCCACGACCCCTGTGGCGGTGAGTGTCTTGAATGAGGAACCTGAGAAAATT 360

QY 361 AATTTCTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Db 361 AATTTCTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420

QY 421 GGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCAATCAGGTAAC 480
Db 421 GGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCAATCAGGTAAC 480

QY 481 TGGGATATCCATCACATCAAAACATTTATTTTATTTCTTTTAGACAGAGTCTCACTCTG 540
Db 481 TGGGATATCCATCACATCAAAACATTTATTTTATTTCTTTTAGACAGAGTCTCACTCTG 540

QY 541 TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT 600
Db 541 TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT 600

QY 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAAT 660
Db 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAAT 660

QY 661 GCCCACTAAATTTTGTATTTTGTAGTAGAGACGGGGTTTGCCATGTTGCCAGGCTGGC 720
Db 661 GCCCACTAAATTTTGTATTTTGTAGTAGAGACGGGGTTTGCCATGTTGCCAGGCTGGC 720

QY 721 CTTGAATCCTGGCCTCAAACAATCCACTTGCCTCGGCTCCCAAGTGTATGATTACA 780
Db 721 CTTGAATCCTGGCCTCAAACAATCCACTTGCCTCGGCTCCCAAGTGTATGATTACA 780

QY 781 GCGGTGAGCCACCGTGCCTGGCCCTAAACATTTATCTTTTCTTTTGTGTTGGGAACTTTGAA 840
Db 781 GCGGTGAGCCACCGTGCCTGGCCCTAAACATTTATCTTTTCTTTTGTGTTGGGAACTTTGAA 840

QY 841 ATTATACAATGAATTTATTTAACTGTCTCCTCGTGTGCTATGGAACACTGGGACT 900
Db 841 ATTATACAATGAATTTATTTAACTGTCTCCTCGTGTGCTATGGAACACTGGGACT 900

QY 901 TCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTTCATCCCCACTC 960
Db 901 TCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTTCATCCCCACTC 960

QY 961 CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC 1020
Db 961 CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC 1020

QY 1021 TTTTGTAGCTCCACATGTGAGTAAGAAAAATGCAATATTTGTCTTTCTGTGCTGCTTAA 1080
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Db 1021 TTTTGTAGCTCCACATGTGAGTAAGAAAAATGCAATATTTGTCTTTCTGTGCTGCTTAA 1080
QY 1081 TTTTACCTTAACATAATGACTTCCCTGTTCCATCCATGTTGTCGCAAAATGACAGGATTCGT 1140
Db 1081 TTTTACCTTAACATAATGACTTCCCTGTTCCATCCATGTTGTCGCAAAATGACAGGATTCGT 1140
QY 1141 TCTTAATTTCAATTAATAATAACACACATGGCAAAA 1177
Db 1141 TCTTAATTTCAATTAATAATAACACACATGGCAAAA 1177

RESULT 8
US-10-208-024-381
; Sequence 381, Application US/10208024
; Publication No. US20040048335A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C538
; CURRENT APPLICATION NUMBER: US/10/208,024
; CURRENT FILING DATE: 2002-07-29
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 381
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-208-024-381
```

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Query Match      100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCTACATGGGCTCCTGCTGCTGGTCTCTTCTCAGCCTCCTGCCGGTGGCTTAC 60
Db 1 AACTTCTACATGGGCTCCTGCTGCTGGTCTCTTCTCAGCCTCCTGCCGGTGGCTTAC 60

QY 61 ACCATCATGTCCCTCCCACCCCTCCTTTGACTGCGGGCCGTTACAGGTGCAGAGTCTCAGTT 120
Db 61 ACCATCATGTCCCTCCCACCCCTCCTTTGACTGCGGGCCGTTACAGGTGCAGAGTCTCAGTT 120
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QY 121 GCCGGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCGAGAATTCCA 180
Db |||||
QY 121 GCCGGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCGAGAATTCCA 180
Db |||||
QY 181 GTTCTGGTTTCATGCCAGCTGTAAAGGCCATGGAACCTTTGGGTGAATCACCGGATGCCA 240
Db GTTCTGGTTTCATGCCAGCTGTAAAGGCCATGGAACCTTTGGGTGAATCACCGGATGCCA 240
QY 241 TTTAAGAGGGTTTTCTGCCAGGATGGAAATGTTAGTCTGTTCTGTCTGCGCTGTTTCAT 300
Db TTTAAGAGGGTTTTCTGCCAGGATGGAAATGTTAGTCTGTTCTGTCTGCGCTGTTTCAT 300
QY 301 TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTCTTGAATGAGGAACCTGAGAAATT 360
Db TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTCTTGAATGAGGAACCTGAGAAATT 360
QY 361 AATTTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Db AATTTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
QY 421 GGGGTACATGTGATATTTGGATACATGTATACAAATATATATATGATCAATCAGGGTAAC 480
Db GGGGTACATGTGATATTTGGATACATGTATACAAATATATATATGATCAATCAGGGTAAC 480
QY 481 TGGGATATCCATCACATCAAAACATTTATTTTTTATCTTTTTTAGACAGAGTCTCACTCG 540
Db TGGGATATCCATCACATCAAAACATTTATTTTTTATCTTTTTTAGACAGAGTCTCACTCG 540
QY 541 TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT 600
Db TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT 600
QY 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGTGGGACTACAGGATGCACCACAAT 660
Db TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGTGGGACTACAGGATGCACCACAAT 660
QY 661 GCCCAACTAATTTTGTATTTTAGTAGAGACGGGTTTTGCCATGTTGCCAGGCTGGC 720
Db GCCCAACTAATTTTGTATTTTAGTAGAGACGGGTTTTGCCATGTTGCCAGGCTGGC 720
QY 721 CTTGAACTCCTGGCCTCAAAACAATCCACTTGCCCTCGGCCTCCCAAGTGTATGATTACA 780
Db CTTGAACTCCTGGCCTCAAAACAATCCACTTGCCCTCGGCCTCCCAAGTGTATGATTACA 780
QY 781 GCGGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTGGAACTTTGAA 840
Db GCGGTGAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTGGAACTTTGAA 840
QY 841 ATTATACAATGAATTAATGTAACTGTCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Db ATTATACAATGAATTAATGTAACTGTCTCCCTGCTGTGCTATGGAACACTGGGACT 900
QY 901 TCTTCCCTCTATCTAATCTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTC 960
Db TCTTCCCTCTATCTAATCTGTATATTTGTACCAGTTAACCAACCGTACTTCATCCCCACTC 960
QY 961 CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC 1020
Db CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC 1020
QY 1021 TTTTITAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTGCTTGGCTTA 1080
Db TTTTITAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTGCTTGGCTTA 1080
QY 1081 TTTCACTTAACATAATGACTTCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTTCGT 1140
Db TTTCACTTAACATAATGACTTCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTTCGT 1140
QY 1141 TCTTAATTTCAATTAATAAACCACACATGGCAAAA 1177
Db TCTTAATTTCAATTAATAAACCACACATGGCAAAA 1177

RESULT 9
US-10-201-853-381
; Sequence 381, Application US/10201853
; Publication No. US20040053358A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3430R1C465
; CURRENT APPLICATION NUMBER: US/10/201,853
; CURRENT FILING DATE: 2002-07-23
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063541
; PRIOR FILING DATE: 1997-10-28
; PRIOR APPLICATION NUMBER: 60/063544
; PRIOR FILING DATE: 1997-10-28
; Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 612
; SEQ ID NO 381
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien

US-10-201-853-381

Query Match 100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCTACATGGGCCTCCTGCTGCTGGTGTCTTTCTCAGCCCTCCTGCCGGTGGCCTAC 60
Db |||||
QY 1 AACTTCTACATGGGCCTCCTGCTGCTGGTGTCTTTCTCAGCCCTCCTGCCGGTGGCCTAC 60
Db |||||
QY 61 ACCATCATGTCCCTCCACCTCCTTTGACTGCGGGCGTTTTCAGGTGCAGAGTCTCAGTT 120
Db |||||
QY 61 ACCATCATGTCCCTCCACCTCCTTTGACTGCGGGCGTTTTCAGGTGCAGAGTCTCAGTT 120
Db |||||
QY 121 GCCGGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCGAGAATTCCA 180
Db |||||
QY 121 GCCGGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCGAGAATTCCA 180
Db |||||
QY 181 GTTCTGGTTTCATGCCAGCTGTAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCA 240
Db |||||
QY 181 GTTCTGGTTTCATGCCAGCTGTAAAGGCCATGGAACCTTTGGGTGAATCACCGATGCCA 240
Db |||||
QY 241 TTTAAGAGGGTTTTCTGCCAGGATGGAAATGTTAGTCTGTTCTGTGTCTGCGCTGTTTCAT 300
Db TTTAAGAGGGTTTTCTGCCAGGATGGAAATGTTAGTCTGTTCTGTGTCTGCGCTGTTTCAT 300

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QY 301 TTCAGTAGCCACGACCCAGCTGTGGCGTTGAGTGTCTGAAATGAGGAACCTGAGAAATTT 360
Db 301 TTCAGTAGCCACGACCCAGCTGTGGCGTTGAGTGTCTGAAATGAGGAACCTGAGAAATTT 360
QY 361 AATTCTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Db 361 AATTCTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
QY 421 GGGGTACATGTGATATTTGGATACATGTATACAAATATATAATGATCAAAATCAGGTAAC 480
Db 421 GGGGTACATGTGATATTTGGATACATGTATACAAATATATAATGATCAAAATCAGGTAAC 480
QY 481 TGGGATATCCATCACATCAAAATTTATTTTATTTCTTTTATAGACAGAGTCTCACTCTG 540
Db 481 TGGGATATCCATCACATCAAAATTTATTTTATTTCTTTTATAGACAGAGTCTCACTCTG 540
QY 541 TCACCCAGGTGGAGTGCAGTGGTGCATCTCAGCTTACTGCAACCTCTGCCCTGCCAGGT 600
Db 541 TCACCCAGGTGGAGTGCAGTGGTGCATCTCAGCTTACTGCAACCTCTGCCCTGCCAGGT 600
QY 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCAAT 660
Db 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCAAT 660
QY 661 GCGCAACTAATTTTGTATTTTATAGTAGAGCGGGTTTGGCCATGTTGCCAGGCTGGC 720
Db 661 GCGCAACTAATTTTGTATTTTATAGTAGAGCGGGTTTGGCCATGTTGCCAGGCTGGC 720
QY 721 CTTGAACCTCTGGCCTCAAAATCCACTTGCCTCGGCCCTCCCAAGTGTATGATTACA 780
Db 721 CTTGAACCTCTGGCCTCAAAATCCACTTGCCTCGGCCCTCCCAAGTGTATGATTACA 780
QY 781 GCGGTAGCCACCGTGCCTGGCCCTAAACATTTATCTTTTCTTTTGTGGAACTTTGAA 840
Db 781 GCGGTAGCCACCGTGCCTGGCCCTAAACATTTATCTTTTCTTTTGTGGAACTTTGAA 840
QY 841 ATTATACATGAATTTATTTGTAATGTAATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Db 841 ATTATACATGAATTTATTTGTAATGTAATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
QY 901 TCTTCCCTCTATCTCAACCTCTGATCACTCTATCTACTCTACTCTACTCTACTCTACTCT 960
Db 901 TCTTCCCTCTATCTCAACCTCTGATCACTCTATCTACTCTACTCTACTCTACTCTACTCT 960
QY 961 CTCTCTATCCTTCCCAACCTCTGATCACTCTATCTACTCTACTCTACTCTACTCTACTCT 1020
Db 961 CTCTCTATCCTTCCCAACCTCTGATCACTCTATCTACTCTACTCTACTCTACTCTACTCT 1020
QY 1021 TTTTGTAGCTCCACATGTGAGTAAGAAATGCAATATTTGTCTTTCTGTGCTGGCTTA 1080
Db 1021 TTTTGTAGCTCCACATGTGAGTAAGAAATGCAATATTTGTCTTTCTGTGCTGGCTTA 1080
QY 1081 TTTCACTTAACATAATGACTTCCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTCGT 1140
Db 1081 TTTCACTTAACATAATGACTTCCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTCGT 1140
QY 1141 TCTTAATTTCAATTAATAATACCAACATGGAATAA 1177
Db 1141 TCTTAATTTCAATTAATAATACCAACATGGAATAA 1177

```

RESULT 10

```

US-10-063-745-129
; Sequence 129, Application US/10063745
; Publication No. US20040058411A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.

```

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; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,745
; CURRENT FILING DATE: 2002-05-09
; Prior Application removed - See Palm or File Wrapper
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 129
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-745-129

```

Query Match 100.0%; Score 1177; DB 13; Length 1177;

Best Local Similarity 100.0%; Pred. No. 9.7e-305;

Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 AACTTCTACATGGGCTCTCTGCTGGTGTCTTCTCAGCCCTCTGCGGCTGGCTAC 60
Db 1 AACTTCTACATGGGCTCTCTGCTGGTGTCTTCTCAGCCCTCTGCGGCTGGCTAC 60
QY 61 ACCATCATGTCCCTCCACCCCTCTTGAAGTGGGCGCTTCAAGTGCAGATCTCAGTT 120
Db 61 ACCATCATGTCCCTCCACCCCTCTTGAAGTGGGCGCTTCAAGTGCAGATCTCAGTT 120
QY 121 GCGCGGAGCACCTCCCTCCGAGGCGAGTCTGTCTCAGAGGCGCTCGGCCAGAAATCCA 180
Db 121 GCGCGGAGCACCTCCCTCCGAGGCGAGTCTGTCTCAGAGGCGCTCGGCCAGAAATCCA 180
QY 181 GTTCTGTTTCATGCCAGCCCTGTAAGAGGCCATGGAATTTGGGTGAATCACCAGTCCA 240
Db 181 GTTCTGTTTCATGCCAGCCCTGTAAGAGGCCATGGAATTTGGGTGAATCACCAGTCCA 240
QY 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGTCTGTCTGTCTGCGCTGTTTCTAT 300
Db 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGTCTGTCTGTCTGCGCTGTTTCTAT 300
QY 301 TTCAGTAGCCACGACCCAGCTGTGGCGTTGAGTGTCTGAAATGAGGAACCTGAGAAATTT 360
Db 301 TTCAGTAGCCACGACCCAGCTGTGGCGTTGAGTGTCTGAAATGAGGAACCTGAGAAATTT 360
QY 361 AATTCTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Db 361 AATTCTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
QY 421 GGGGTACATGTGATATTTGGATACATGTATACAAATATATAATGATCAAAATCAGGTAAC 480
Db 421 GGGGTACATGTGATATTTGGATACATGTATACAAATATATAATGATCAAAATCAGGTAAC 480
QY 481 TGGGATATCCATCACATCAAAATTTATTTTATTTTCTTTTATAGACAGAGTCTCACTCTG 540
Db 481 TGGGATATCCATCACATCAAAATTTATTTTATTTTCTTTTATAGACAGAGTCTCACTCTG 540
QY 541 TCACCCAGGTGGAGTGCAGTGGTGCATCTCAGCTTACTGCAACCTCTGCCCTGCCAGGT 600
Db 541 TCACCCAGGTGGAGTGCAGTGGTGCATCTCAGCTTACTGCAACCTCTGCCCTGCCAGGT 600
QY 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCAAT 660
Db 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCAAT 660
QY 661 GCCCAACTAATTTTGTATTTTATAGTAGAGCGGGTTTGGCCATGTTGCCAGGCTGGC 720
Db 661 GCCCAACTAATTTTGTATTTTATAGTAGAGCGGGTTTGGCCATGTTGCCAGGCTGGC 720
QY 721 CTTGAACCTCTGGCCTCAAAATCCACTTGCCTCGGCCCTCCCAAGTGTATGATTACA 780
Db 721 CTTGAACCTCTGGCCTCAAAATCCACTTGCCTCGGCCCTCCCAAGTGTATGATTACA 780
QY 781 GCGGTAGCCACCGTGCCTGGCCCTAAACATTTATCTTTTCTTTTGTGGAACTTTGAA 840

```


Db 781 GCGGTGAGCCACCGTGGCGCTAAACATTTATCTTTTCTTTGTGTGGGAACCTTTGAA 840
Qy 841 ATTATACAATGAATATTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Db 841 ATTATACAATGAATATTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Qy 901 TCTTCCCTCTATCTAACTGTATATTTGTACCAAGTTAAACCAACCGTACTTTCATCCCACTC 960
Db 901 TCTTCCCTCTATCTAACTGTATATTTGTACCAAGTTAAACCAACCGTACTTTCATCCCACTC 960
Qy 961 CTCTCTATCCTTCCCAACCTCTGTATCACTCTACTTCTACTCTCTACCTCCATGAGATCCAC 1020
Db 961 CTCTCTATCCTTCCCAACCTCTGTATCACTCTACTTCTACTCTCTACCTCCATGAGATCCAC 1020
Qy 1021 TTTTGTAGCTCCCAACATGTGAGTAAGAAAATGCAATATTGTCTTTCTGTGCGCTGCTTA 1080
Db 1021 TTTTGTAGCTCCCAACATGTGAGTAAGAAAATGCAATATTGTCTTTCTGTGCGCTGCTTA 1080
Qy 1081 TTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTCGT 1140
Db 1081 TTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTCGT 1140
Qy 1141 TCTTAATTTCAATTTAAATAACCAACACATGGCAAAAA 1177
Db 1141 TCTTAATTTCAATTTAAATAACCAACACATGGCAAAAA 1177

RESULT 11

US-10-063-512-129
; Sequence 129, Application US/10063512
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,512
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 129
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-512-129

Query Match 100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 AACTTCTACATGGGCTCCTGCTGGTGCTCTTCTCAGCCTCCTGCGGTGGCCTAC 60
Db 1 AACTTCTACATGGGCTCCTGCTGGTGCTCTTCTCAGCCTCCTGCGGTGGCCTAC 60
Qy 61 ACCATCATGTCCTCCCAACCTCTTTGACTGCGGGCGGTTGAGTGCAGAGTCTCAGTT 120
Db 61 ACCATCATGTCCTCCCAACCTCTTTGACTGCGGGCGGTTGAGTGCAGAGTCTCAGTT 120
Qy 121 GCCGGGAGCACCTCCCTCCGAGGCAGTCTGTCTAGAGGGCCCTCGGCCCAAGATTCCA 180
Db 121 GCCGGGAGCACCTCCCTCCGAGGCAGTCTGTCTAGAGGGCCCTCGGCCCAAGATTCCA 180
Qy 181 GTTCTGGTTTCATGCCAGCCTGTAAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCA 240
Db 181 GTTCTGGTTTCATGCCAGCCTGTAAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCA 240

RESULT 12
US-10-063-513-129
; Sequence 129, Application US/10063513
; Publication No. US20030018172A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen

Qy 241 TTTAAGAGGGTTTTCTGCCAGATGGAATGTTAGTTCGTTCTGTCTCGGCTGTTCAT 300
Db 241 TTTAAGAGGGTTTTCTGCCAGATGGAATGTTAGTTCGTTCTGTCTCGGCTGTTCAT 300
Qy 301 TTCAGTAGCCACAGCCACCTGTGGCCGTTGAGTGCITGAAATGAGGAACCTGAGAAAATT 360
Db 301 TTCAGTAGCCACAGCCACCTGTGGCCGTTGAGTGCITGAAATGAGGAACCTGAGAAAATT 360
Qy 361 AATTCTCATGTATTTTCTCAATTTATTATTATTATTATTATTATTATTATTATTATT 420
Db 361 AATTCTCATGTATTTTCTCAATTTATTATTATTATTATTATTATTATTATTATTATT 420
Qy 421 GGGGTACATGTGATATTGATATACATGTATATACAATATATAATGATCAAAATCAGGGTAAC 480
Db 421 GGGGTACATGTGATATTGATATACATGTATATACAATATATAATGATCAAAATCAGGGTAAC 480
Qy 481 TGGGATATCCATCACATCAACATTTATTTTATTCTTTTATAGACAGAGTCTCACTCTG 540
Db 481 TGGGATATCCATCACATCAACATTTATTTTATTCTTTTATAGACAGAGTCTCACTCTG 540
Qy 541 TCACCCAGGCTGGAGTGCAGTGGTGCCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT 600
Db 541 TCACCCAGGCTGGAGTGCAGTGGTGCCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGT 600
Qy 601 TCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAAT 660
Db 601 TCAAGCGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAAT 660
Qy 661 GCCCAACTAATTTTGTATTTTAGTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGC 720
Db 661 GCCCAACTAATTTTGTATTTTAGTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGC 720
Qy 721 CTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCTCCCAAGTGTATGATTACA 780
Db 721 CTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCTCCCAAGTGTATGATTACA 780
Qy 781 GGCGTGAGCCACCGTGGCGCTAAACATTTATCTTTTGTGTGGGAACCTTTGAA 840
Db 781 GGCGTGAGCCACCGTGGCGCTAAACATTTATCTTTTGTGTGGGAACCTTTGAA 840
Qy 841 ATTATACAATGAATATTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Db 841 ATTATACAATGAATATTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Qy 901 TCTTCCCTCTATCTAACTGTATATTTGTACCAAGTTAAACCCGTTAACCCGTTACTTCCCACTC 960
Db 901 TCTTCCCTCTATCTAACTGTATATTTGTACCAAGTTAAACCCGTTACTTCCCACTC 960
Qy 961 CTCTCTATCCTTCCCAACCTCTGTATCACTCTACTCTCTACTCTCTATGAGATCCAC 1020
Db 961 CTCTCTATCCTTCCCAACCTCTGTATCACTCTACTCTCTACTCTCTATGAGATCCAC 1020
Qy 1021 TTTTGTAGCTCCCAACATGTGAGTAAGAAAATGCAATATTGTTCTGTGCGCTGCTTA 1080
Db 1021 TTTTGTAGCTCCCAACATGTGAGTAAGAAAATGCAATATTGTTCTTTCTGTGCGCTGCTTA 1080
Qy 1081 TTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTCGT 1140
Db 1081 TTTCACTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTCGT 1140
Qy 1141 TCTTAATTTCAATTTAAATAACCAACACATGGCAAAAA 1177
Db 1141 TCTTAATTTCAATTTAAATAACCAACACATGGCAAAAA 1177

; APPLICANT: Gerritsen,Mary E.
; APPLICANT: Goddard,Audrey
; APPLICANT: Godowski,Paul J.
; APPLICANT: Grimaldi,Christopher J.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Gurney,Austin L.
; APPLICANT: Watanabe,Colin K.
; APPLICANT: Wood,William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,513
; CURRENT FILING DATE: 2002-05-01
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 129
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-513-129

Query Match 100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCTACATGGGCGCTCCTGCTGCTGGTCTCTTCTCAGCCTCCTGCGGTGGCTAC 60
Db 1 AACTTCTACATGGGCGCTCCTGCTGCTGGTCTCTTCTCAGCCTCCTGCGGTGGCTAC 60

QY 61 ACCATCATGTCCCTCCACCCCTCCTTTGACTGCGGGCGGTTTTCAGGTGCAGAGTCTCAGTT 120
Db 61 ACCATCATGTCCCTCCACCCCTCCTTTGACTGCGGGCGGTTTTCAGGTGCAGAGTCTCAGTT 120

QY 121 GCGCGGAGCAGCTCCCTCCAGGAGTCTGCTCAGAGGCGCTCGGCCAGAAATCCA 180
Db 121 GCGCGGAGCAGCTCCCTCCAGGAGTCTGCTCAGAGGCGCTCGGCCAGAAATCCA 180

QY 181 GTTCTGTTTCATGCCAGCTGTAAAGGCCATGGAACCTTTGGTGAATCACCGATGCCA 240
Db 181 GTTCTGTTTCATGCCAGCTGTAAAGGCCATGGAACCTTTGGTGAATCACCGATGCCA 240

QY 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGTCTGTTCTGTTCTGCGCTGTTTCAT 300
Db 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGTCTGTTCTGTTCTGCGCTGTTTCAT 300

QY 301 TTCAGTAGCCAGCCAGCCCTGTGSCCGTTGAGTCTTGAATGAGGAAGTGAAGAAATTT 360
Db 301 TTCAGTAGCCAGCCAGCCCTGTGSCCGTTGAGTCTTGAATGAGGAAGTGAAGAAATTT 360

QY 361 AATTTCTCATGTATTTTCTCATTTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Db 361 AATTTCTCATGTATTTTCTCATTTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420

QY 421 GGGGGTACATGTGATATTTGGATACATGTATACAAATATATATGATCAAATCAGGGTAAC 480
Db 421 GGGGGTACATGTGATATTTGGATACATGTATACAAATATATATGATCAAATCAGGGTAAC 480

QY 481 TGGGATATCCATCACATCAAACATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 540
Db 481 TGGGATATCCATCACATCAAACATTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 540

QY 541 TCACCCAGGCTGGAGTGCACTGCGGCTCAGCTTCTGCAACCTCTGCGCTGCCAGGT 600
Db 541 TCACCCAGGCTGGAGTGCACTGCGGCTCAGCTTCTGCAACCTCTGCGCTGCCAGGT 600

QY 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCCACAAT 660
Db 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCCACAAT 660

QY 661 GCCCAACTAATTTTGTATTTTGTAGTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGC 720
Db 661 GCCCAACTAATTTTGTATTTTGTAGTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGC 720

QY 721 CTTGAATCCTGGCCTCAAACAATCCACTTGCCTCGGCCCTCCCAAGTGTATGATTACA 780

Db 721 CTTGAATCCTGGCCTCAAACAATCCACTTGCCTCGGCCCTCCCAAGTGTATGATTACA 780
QY 781 GCGGTGAGCCACCGTGCCTGGCCCTAAACATTTATCTTTTCTTGTGTGGAACTTTGAA 840
Db 781 GCGGTGAGCCACCGTGCCTGGCCCTAAACATTTATCTTTTCTTGTGTGGAACTTTGAA 840
QY 841 ATTATACAATGAATTTATTGTTAACTGTCTATCTCCCTGCTGTCTATGGAACACTGGGACT 900
Db 841 ATTATACAATGAATTTATTGTTAACTGTCTATCTCCCTGCTGTCTATGGAACACTGGGACT 900
QY 901 TCTTCCCTCTATCTAACTGTATATTGTACCAAGTTAACCAACCGTACTTTCATCCCCACTC 960
Db 901 TCTTCCCTCTATCTAACTGTATATTGTACCAAGTTAACCAACCGTACTTTCATCCCCACTC 960
QY 961 CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC 1020
Db 961 CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC 1020
QY 1021 TTTTGTAGCTCCACATGTGAGTAAGAAAAATGCAATATTGTCTTTCTGTGCTGGCTTA 1080
Db 1021 TTTTGTAGCTCCACATGTGAGTAAGAAAAATGCAATATTGTCTTTCTGTGCTGGCTTA 1080
QY 1081 TTTCACTTAACATAATGACTTCCCTGTTCCATCCATGTTGTCGCAAAATGACAGGATTCGT 1140
Db 1081 TTTCACTTAACATAATGACTTCCCTGTTCCATCCATGTTGTCGCAAAATGACAGGATTCGT 1140
QY 1141 TCTTAATTTCAATTAATAATACCAACATGGCAAAA 1177
Db 1141 TCTTAATTTCAATTAATAATACCAACATGGCAAAA 1177

RESULT 13
US-10-063-569-129
; Sequence 129, Application US/10063569
; Publication No. US20030018168A1
; GENERAL INFORMATION:
; APPLICANT: Eaton,Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; TITLE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,569
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 129
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-569-129

Query Match 100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCTACATGGGCGCTCCTGCTGCTGGTCTCTTCTCAGCCTCCTGCGGTGGCTAC 60
Db 1 AACTTCTACATGGGCGCTCCTGCTGCTGGTCTCTTCTCAGCCTCCTGCGGTGGCTAC 60

QY 61 ACCATCATGTCCCTCCACCCCTCCTTTGACTGCGGGCGGTTTTCAGGTGCAGAGTCTCAGTT 120
Db 61 ACCATCATGTCCCTCCACCCCTCCTTTGACTGCGGGCGGTTTTCAGGTGCAGAGTCTCAGTT 120

QY 121 GCGCGGAGCAGCTCCCTCCAGGAGTCTGCTCAGAGGCGCTCGGCCAGAAATCCA 180

Db 121 GCCCGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCTCGGCCCGAGAATTCCA 180
Qy 181 GTTCGGTTTCATGCCAGCCTGTAAAGGCCCATGGAACTTTGGGTGAATCACCAGTGCCA 240
Db 181 GTTCGGTTTCATGCCAGCCTGTAAAGGCCCATGGAACTTTGGGTGAATCACCAGTGCCA 240
Qy 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGGTCGTTCTGTCTCGCTGTTTCAT 300
Db 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGGTCGTTCTGTCTCGCTGTTTCAT 300
Qy 301 TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGCCTTGAATGAGGAACCTGAGAAAATT 360
Db 301 TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGCCTTGAATGAGGAACCTGAGAAAATT 360
Qy 361 AATTTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Db 361 AATTTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Qy 421 GGGGTACATGTGATATTTTGGATACATGTATACAATATATAATGATCAAAATCAGGGTAAC 480
Db 421 GGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCAAAATCAGGGTAAC 480
Qy 481 TGGATATCCATCACATCAAAACATTTATTTTATTTCTTTTATAGACAGAGTCTCACTCTG 540
Db 481 TGGATATCCATCACATCAAAACATTTATTTTATTTCTTTTATAGACAGAGTCTCACTCTG 540
Qy 541 TCACCCAGGCTGGAGTGCAGTGGTGCCTCACTCTCAGCTTACTGCAACCTCTGCCAGGT 600
Db 541 TCACCCAGGCTGGAGTGCAGTGGTGCCTCACTCTCAGCTTACTGCAACCTCTGCCAGGT 600
Qy 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGACTACAGGCAATGACCCACAAT 660
Db 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGACTACAGGCAATGACCCACAAT 660
Qy 661 GCCCAACTAATTTTGTATTTTAGTAGAGACGGGTTTGCCATGTTGCCAGGCTGGC 720
Db 661 GCCCAACTAATTTTGTATTTTAGTAGAGACGGGTTTGCCATGTTGCCAGGCTGGC 720
Qy 721 CTTGAACCTCGCCTCAAAACAATCCACTTGCCCTCGGCTCCCAAGTGTATGATTACA 780
Db 721 CTTGAACCTCGCCTCAAAACAATCCACTTGCCCTCGGCTCCCAAGTGTATGATTACA 780
Qy 781 GGGGTAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGAACTTTGAA 840
Db 781 GGGGTAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTTGGAACTTTGAA 840
Qy 841 ATTATACAATGAATTATTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Db 841 ATTATACAATGAATTATTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGGACT 900
Qy 901 TCTTCCCTCTATCTAACTGTATATTTGTACCAGTTTAAACCAACCGTACTTCTATCCCCACTC 960
Db 901 TCTTCCCTCTATCTAACTGTATATTTGTACCAGTTTAAACCAACCGTACTTCTATCCCCACTC 960
Qy 961 CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC 1020
Db 961 CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC 1020
Qy 1021 TTTTGTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTGCTGGCTTA 1080
Db 1021 TTTTGTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTGCTGGCTTA 1080
Qy 1081 TTTCACTTAACATAATGACTTCCTGTTCCATCCATGCTGCAATGACAGATTTTCGT 1140
Db 1081 TTTCACTTAACATAATGACTTCCTGTTCCATCCATGCTGCAATGACAGATTTTCGT 1140
Qy 1141 TCTTAATTTCAATTAATAAACCACACATGGCAAAA 1177
Db 1141 TCTTAATTTCAATTAATAAACCACACATGGCAAAA 1177

; Sequence 129, Application US/10063551
; Publication No. US20020183494A1
; GENERAL INFORMATION:
; APPLICANT: Eaton, Dan L.
; APPLICANT: Filvaroff, Ellen
; APPLICANT: Gerritsen, Mary E.
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Grimaldi, Christopher J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE OF INVENTION: ACIDS ENCODING THE SAME
; FILE REFERENCE: P3230R1C1
; CURRENT APPLICATION NUMBER: US/10/063,551
; CURRENT FILING DATE: 2002-05-02
; Prior Application removed - See File Wrapper or Palm
; NUMBER OF SEQ ID NOS: 170
; SEQ ID NO 129
; LENGTH: 1177
; TYPE: DNA
; ORGANISM: Homo Sapien
US-10-063-551-129

Query Match 100.0%; Score 1177; DB 13; Length 1177;

Best Local Similarity 100.0%; Pred. No. 9.7e-305;

Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 AACTTCTACATGGGCCTCCTGCTGCTGCTCTTCTCAGCCCTCCTGCCGTTGCCCTAC 60
Db 1 AACTTCTACATGGGCCTCCTGCTGCTGCTCTTCTCAGCCCTCCTGCCGTTGCCCTAC 60
Qy 61 ACCATCATGTCCCTCCCACCCCTCTTTGACTGCGGGCCGTTCAGGTGCAGAGTCTCAGTT 120
Db 61 ACCATCATGTCCCTCCCACCCCTCTTTGACTGCGGGCCGTTCAGGTGCAGAGTCTCAGTT 120
Qy 121 GCCCGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGCCCTCGGCCCGAGAATTCCA 180
Db 121 GCCCGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGCCCTCGGCCCGAGAATTCCA 180
Qy 181 GTTCTGTTTCATGCCAGCCTGTAAAGGCCCATGGAACTTTGGGTGAATCACCAGTGCCA 240
Db 181 GTTCTGTTTCATGCCAGCCTGTAAAGGCCCATGGAACTTTGGGTGAATCACCAGTGCCA 240
Qy 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGGTCTGTCTGTCTGCGCTGTTTCAT 300
Db 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGGTCTGTCTGTCTGCGCTGTTTCAT 300
Qy 301 TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGCCTTGAATGAGGAACCTGAGAAAATT 360
Db 301 TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGCCTTGAATGAGGAACCTGAGAAAATT 360
Qy 361 AATTTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Db 361 AATTTCATGTATTTTCTCATTTATTTATTAATTTTAACTGATAGTTGTACATATTT 420
Qy 421 GGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCAAAATCAGGGTAAC 480
Db 421 GGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCAAAATCAGGGTAAC 480
Qy 481 TGGGATATCCATCACATCAAAACATTTATTTTATTTTATAGACAGAGTCTCACTCTG 540
Db 481 TGGGATATCCATCACATCAAAACATTTATTTTATTTTATAGACAGAGTCTCACTCTG 540
Qy 541 TCACCCAGGCTGGAGTGCAGTGGTGCCTCTCAGCTTACTGCAACCTCTGCCGTCAGGT 600
Db 541 TCACCCAGGCTGGAGTGCAGTGGTGCCTCTCAGCTTACTGCAACCTCTGCCGTCAGGT 600
Qy 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCAATGACCCACAAT 660
Db 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCAATGACCCACAAT 660

QY	661	GCCCAACTAATTTTGTATTTTAGTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGC	720
DB	661		720
QY	721	CTTGAACCTCCTGGCCTCAAAACAATCCACTTGCCTCGGCCCTCCCAAAGTGTATGATTACA	780
DB	721		780
QY	781	GGCGTGAGCCACCGTGCCCTGGCCATAACATTTATCTTTCTTTGTGTTGGGAACCTTTGAA	840
DB	781		840
QY	841	ATTATACAAATGAATTATTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACTGGGACT	900
DB	841		900
QY	901	TCTTCCCTCTATCTAACTGTATATTTGTACCAGTTAACCAACCGTACTTTCATCCCCACTC	960
DB	901		960
QY	961	CTCTCTATCCTTCCCAACCTCTGTATCACTTCTACTCTCTACCTCCATGAGATCCAC	1020
DB	961		1020
QY	1021	TTTTTTAGCTCCACATGTGAGTAAGAAAAATGCAATATTTGTCTTTCTGTGCTGGCTTA	1080
DB	1021		1080
QY	1081	TTTCACCTTAACATAATGACTTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTCTGT	1140
DB	1081		1140
QY	1141	TCTTAATTTCAATTAATAAACCACACATGGCAAAAA	1177
DB	1141		1177

RESULT 15

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US-10-174-581-381
; Sequence 381, Application US/10174581
; Publication No. US20030017540A1
; GENERAL INFORMATION:
; APPLICANT: Baker, Kevin P.
; APPLICANT: Chen, Jian
; APPLICANT: Desnoyers, Luc
; APPLICANT: Goddard, Audrey
; APPLICANT: Godowski, Paul J.
; APPLICANT: Gurney, Austin L.
; APPLICANT: Pan, James
; APPLICANT: Smith, Victoria
; APPLICANT: Watanabe, Colin K.
; APPLICANT: Wood, William I.
; APPLICANT: Zhang, Zemin
; TITLE OF INVENTION: SECRETED AND TRANSMEMBRANE POLYPEPTIDES AND NUCLEIC
; FILE REFERENCE: P3430R1C41
; CURRENT APPLICATION NUMBER: US/10/174,581
; CURRENT FILING DATE: 2002-06-18
; PRIOR APPLICATION NUMBER: 10/052586
; PRIOR FILING DATE: 2002-01-15
; PRIOR APPLICATION NUMBER: 60/059263
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/059266
; PRIOR FILING DATE: 1997-09-18
; PRIOR APPLICATION NUMBER: 60/062250
; PRIOR FILING DATE: 1997-10-17
; PRIOR APPLICATION NUMBER: 60/063120
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063121
; PRIOR FILING DATE: 1997-10-24
; PRIOR APPLICATION NUMBER: 60/063486
; PRIOR FILING DATE: 1997-10-21
; PRIOR APPLICATION NUMBER: 60/063540

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;
; PRIOR APPLICATION NUMBER: 60/083499
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/083559
; PRIOR FILING DATE: 1998-04-29
; PRIOR APPLICATION NUMBER: 60/084366
; PRIOR FILING DATE: 1998-05-05
; PRIOR APPLICATION NUMBER: 60/084414
; PRIOR FILING DATE: 1998-05-06
; PRIOR APPLICATION NUMBER: 60/084639
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084640
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/084643
; PRIOR FILING DATE: 1998-05-07
; PRIOR APPLICATION NUMBER: 60/085573
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085579
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085580
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085582
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/085700
; PRIOR FILING DATE: 1998-05-15
; PRIOR APPLICATION NUMBER: 60/086023
; PRIOR FILING DATE: 1998-05-18
; PRIOR APPLICATION NUMBER: 60/086392
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/086486
; PRIOR FILING DATE: 1998-05-22
; PRIOR APPLICATION NUMBER: 60/087098
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087208
; PRIOR FILING DATE: 1998-05-28
; PRIOR APPLICATION NUMBER: 60/087609
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087759
; PRIOR FILING DATE: 1998-06-02
; PRIOR APPLICATION NUMBER: 60/087827
; PRIOR FILING DATE: 1998-06-03
; PRIOR APPLICATION NUMBER: 60/088025
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088028
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088029
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088033
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088167
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088202
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088212
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088217
; PRIOR FILING DATE: 1998-06-05
; PRIOR APPLICATION NUMBER: 60/088326
; PRIOR FILING DATE: 1998-06-04
; PRIOR APPLICATION NUMBER: 60/088655
; PRIOR FILING DATE: 1998-06-09
; PRIOR APPLICATION NUMBER: 60/088722
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088738
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088740
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088811
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088824
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088825
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088826

;
; PRIOR FILING DATE: 1998-06-10
; PRIOR APPLICATION NUMBER: 60/088861
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088863
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/088876
; PRIOR FILING DATE: 1998-06-11
; PRIOR APPLICATION NUMBER: 60/089090
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089105
; PRIOR FILING DATE: 1998-06-12
; PRIOR APPLICATION NUMBER: 60/089512
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089514
; PRIOR FILING DATE: 1998-06-16
; PRIOR APPLICATION NUMBER: 60/089538
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089598
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: 60/089653

Query Match 100.0%; Score 1177; DB 13; Length 1177;
Best Local Similarity 100.0%; Pred. No. 9.7e-305;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 AACTTCTACATGGGCCTCCTGCTGTGGTCTCTTCCTCAGCCTCTCTGCGGTGGCCTAC 60
Db |||||
1 AACTTCTACATGGGCCTCCTGCTGTGGTCTCTTCCTCAGCCTCTCTGCGGTGGCCTAC 60
QY 61 ACCATCATGTCCCTCCACCCCTCCTTGACTCGGGCCGTTTCCAGGTGCAGAGTCTCAGTT 120
Db |||||
61 ACCATCATGTCCCTCCACCCCTCCTTGACTCGGGCCGTTTCCAGGTGCAGAGTCTCAGTT 120
QY 121 GCGCGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGSCCTCGGCCCAGAAATCCA 180
Db |||||
121 GCGCGGAGCACCTCCCTCCCGAGGCAGTCTGCTCAGAGGSCCTCGGCCCAGAAATCCA 180
QY 181 GTTCTGTTTCATGCCAGCCTGTAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCA 240
Db |||||
181 GTTCTGTTTCATGCCAGCCTGTAAAGGCCATGGAACCTTGGGTGAATCACCGATGCCA 240
QY 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGGTGTTCTGTGTCTGCGCTGTTTCAT 300
Db |||||
241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGGTGTTCTGTGTCTGCGCTGTTTCAT 300
QY 301 TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGCTTGAATGAGGAACTGAGAAATTT 360
Db |||||
301 TTCAGTAGCCACCAGCCACCTGTGGCCGTTGAGTGCTTGAATGAGGAACTGAGAAATTT 360
QY 361 AATTTCTCATGTATTTTCTCATTTTATTATTTAATTTTAACTGATAGTTGTACATATTT 420
Db |||||
361 AATTTCTCATGTATTTTCTCATTTTATTATTTAATTTTAACTGATAGTTGTACATATTT 420
QY 421 GGGGTACATGTGATATTTGGATACATGTATACAATATAATGATCAAAATCAGGTAAC 480
Db |||||
421 GGGGTACATGTGATATTTGGATACATGTATACAATATAATGATCAAAATCAGGTAAC 480
QY 481 TGGGATATCCATCACATCAACATTTATTTTATTTTATTTTAGACAGAGTCTCACTCTG 540
Db |||||
481 TGGGATATCCATCACATCAACATTTATTTTATTTTATTTTAGACAGAGTCTCACTCTG 540
QY 541 TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCGTGCAGGT 600
Db |||||
541 TCACCCAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCGTGCAGGT 600
QY 601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCCACAAT 660
Db |||||
601 TCAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCCACAAT 660
QY 661 GCCCAACTAATTTTGTATTTTAGTAGAGACGGGTTTGGCCATGTTGCCAGGCTGGC 720
Db |||||
661 GCCCAACTAATTTTGTATTTTAGTAGAGACGGGTTTGGCCATGTTGCCAGGCTGGC 720

QY	721	CTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCCTCCCAAAGTGTATGATTACA	780
Db	721	CTTGAACTCCTGGCCTCAAACAATCCACTTGCCCTCGGCCCTCCCAAAGTGTATGATTACA	780
QY	781	GGCGTGAGCCACCGTGCCCTGGCCTAAACATTTATCTTTCTTTGTGTTGGAACTTTGAA	840
Db	781	GGCGTGAGCCACCGTGCCCTGGCCTAAACATTTATCTTTCTTTGTGTTGGAACTTTGAA	840
QY	841	ATTATACAATGAATATTGTTAACTGTGCTATCCCTGCTGTGCTATGGAACACTGGGACT	900
Db	841	ATTATACAATGAATATTGTTAACTGTGCTATCCCTGCTGTGCTATGGAACACTGGGACT	900
QY	901	TCTTCCCTCTATCTAACTGTATATTGTACCAAGTTAACCAACCGTACTTCAATCCCCACTC	960
Db	901	TCTTCCCTCTATCTAACTGTATATTGTACCAAGTTAACCAACCGTACTTCAATCCCCACTC	960
QY	961	CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC	1020
Db	961	CTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTCTACCTCCATGAGATCCAC	1020
QY	1021	TTTTTTAGCTCCACATGTGAGTAAGAAATGCAATATTGTCTTCTGTGCTGGCTTA	1080
Db	1021	TTTTTTAGCTCCACATGTGAGTAAGAAATGCAATATTGTCTTCTGTGCTGGCTTA	1080
QY	1081	TTTCACCTTAACATAATGACTTCCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTT	1140
Db	1081	TTTCACCTTAACATAATGACTTCCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTT	1140
QY	1141	TCTTAATTTCAATTAATAAATAACCAACATGGCAAAA	1177
Db	1141	TCTTAATTTCAATTAATAAATAACCAACATGGCAAAA	1177

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 17:48:17 ; Search time 112 Seconds
(without alignments)
5831.939 Million cell updates/sec

Title: US-10-063-736-129
Perfect score: 1177
Sequence: 1 aactctacatgggcctcct.....ataaccacacatggcaaaaa 1177

Scoring table: IDENTITY NUC
Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents_NA.*
1: /cgn2_6/ptodata/2/ina/5A_COMB.seq.*
2: /cgn2_6/ptodata/2/ina/5B_COMB.seq.*
3: /cgn2_6/ptodata/2/ina/6A_COMB.seq.*
4: /cgn2_6/ptodata/2/ina/6B_COMB.seq.*
5: /cgn2_6/ptodata/2/ina/PCITUS_COMB.seq.*
6: /cgn2_6/ptodata/2/ina/backfiles1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	252.8	21.5	12047	2	US-09-022-461-1
2	252.8	21.5	12047	4	US-09-033-556-3
3	252.8	21.5	12047	4	US-09-474-699-11
4	252.8	21.5	12047	4	US-09-151-376-3
5	233.8	19.9	99916	4	US-09-816-095-3
6	233	19.8	313	4	US-09-621-976-13292
7	232.4	19.7	22976	4	US-09-269-939A-19
8	232.4	19.7	23187	4	US-09-499-522-1
9	231.2	19.6	99500	4	US-09-798-096-10
10	229.2	19.5	246240	2	US-08-724-394A-20
11	229.2	19.5	246240	2	US-08-724-394A-21
12	229.2	19.5	246240	2	US-08-724-394A-22
13	228.8	19.4	128779	4	US-09-497-855A-38
14	228.6	19.4	39982	4	US-09-820-924-3
15	228.2	19.4	21721	4	US-09-269-939A-41
16	227.8	19.4	21968	4	US-09-851-985-3
17	227.2	19.3	48763	4	US-09-916-204-3
18	227.2	19.3	174493	4	US-09-804-471A-3
19	227.2	19.3	174493	4	US-10-238-709-3
20	226.4	19.2	2457	4	US-09-620-312D-223
21	226.2	19.2	80246	3	US-09-078-294-4
22	225	19.1	399	4	US-09-621-976-13959
23	224.6	19.1	1988	2	US-08-257-963B-11
24	224.6	19.1	1988	4	US-08-367-841A-11
25	224.6	19.1	1988	5	PCT-US95-07201-11
26	224.6	19.1	5262	4	US-08-520-373D-5
27	224.6	19.1	22481	4	US-08-367-841A-43

28	224.6	19.1	22481	5	PCT-US95-07201-43
29	224.6	19.1	22484	4	US-09-875-223-2
30	224.6	19.1	22484	4	US-09-875-114-2
31	224.4	19.1	53526	3	US-08-658-136-2
32	224.4	19.1	53577	3	US-08-658-136-1
33	224.4	19.1	118067	4	US-09-497-855A-32
34	224.2	19.0	70000	4	US-09-851-896-3
35	223.8	19.0	1912	4	US-09-800-729-32
36	223.6	19.0	2741	1	US-08-832-883-59
37	223.6	19.0	2741	2	US-08-832-877-59
38	223.6	19.0	41684	4	US-09-536-059-1
39	223.4	19.0	368	4	US-09-621-976-10146
40	223.4	19.0	53332	4	US-09-801-861-3
41	222.8	18.9	498	4	US-09-608-285A-59
42	222.8	18.9	15977	4	US-09-245-281-44
43	222.8	18.9	32042	4	US-09-340-620A-63
44	222.8	18.9	32042	4	US-09-340-620A-63
45	222.8	18.9	392000	4	US-10-027-983-11

ALIGNMENTS

RESULT 1
US-09-022-461-1
; Sequence 1, Application US/09022461
; Patent No. 5964371
; GENERAL INFORMATION:
; APPLICANT: HENDERSON, Daniel R.
; APPLICANT: SCHUUR, Eric R.
; APPLICANT: LAMPARSKI, Henry G.
; APPLICANT: YU, De Chao
; TITLE OF INVENTION: PROSTATE CANCER DRUG SCORE
; TITLE OF INVENTION: ENING
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: MORRISON & FOERSTER
; STREET: 755 PAGE MILL ROAD
; CITY: Palo Alto
; STATE: CA
; COUNTRY: USA
; ZIP: 94304-1018
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/022,461
; FILING DATE: 12-FEB-1998
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/906,192
; FILING DATE: 04-AUG-1997
; ATTORNEY/AGENT INFORMATION:
; NAME: Catherine, Polizzi M
; REGISTRATION NUMBER: 40,130
; REFERENCE/DOCKET NUMBER: 34802-20003.21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-813-5600
; TELEFAX: 415-494-0792
; TELEX: 706141
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12047 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
US-09-022-461-1

Query Match 21.5%; Score 252.8; DB 2; Length 12047;
Best Local Similarity 64.2%; Pred. No. 3.1e-61;
Matches 429; Conservative 0; Mismatches 232; Indels 7; Gaps 3;

Db 2392 ATTTTCA 2399

RESULT 3

US-09-474-699-11

; Sequence 11, Application US/09474699

; Patent No. 6495130

; GENERAL INFORMATION:

; APPLICANT: Henderson, Daniel R.

; APPLICANT: Yu, De Chao

; TITLE OF INVENTION: TARGET CELL-SPECIFIC ADENOVIRAL VECTORS

; TITLE OF INVENTION: CONTAINING E3 AND METHODS OF USE THEREOF

; FILE REFERENCE: 348022001300

; CURRENT APPLICATION NUMBER: US/09/474,699

; CURRENT FILING DATE: 1999-12-29

; PRIOR APPLICATION NUMBER: 60/114,262

; PRIOR FILING DATE: 1998-12-30

; NUMBER OF SEQ ID NOS: 23

; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 11

; LENGTH: 12047

; TYPE: DNA

; ORGANISM: Homo Sapien

US-09-474-699-11

Query Match 21.5%; Score 252.8; DB 4; Length 12047;

Best Local Similarity 64.2%; Pred. No. 3.1e-61;

Matches 429; Conservative 0; Mismatches 232; Indels 7; Gaps 3;

QY 478 AACTGGGATATCCATCACAATCAAAACATTTATTTTATTTTATTTTATGACAGAGTCTCACT 537

Db 1739 AAATGGTCTCCTCACTTTATTTATTTATTTATTTATTTAGATGGAGCCTCGCT 1798

QY 538 CTGTCAACCCAGGCTGGAGTGCAGTGGTGCCTACTCAGCTTACTGCAACCTCTGCCTGCCA 597

Db 1799 CTGTCTCCTAGGCTGGAGTGCATAGTGCATACCA-CTCACTGCAACCTCTGCCTCCTC 1857

QY 598 GGTTCAAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGATGCACCCAC 657

Db 1858 TGTTCAAAGTGATTTTCTTACCTCAGCCTCCCGAGTAGCTGGATTACAGGTGCGTGCCAC 1917

QY 658 AATGCCCAACTAATTTTGTATTTTGTAGTAGAGCGGGTTTGGCCATGTTGCCAGGCT 717

Db 1918 CACACCCGGCTAATTTTGTATTTTGTAGTAGAGCGGGTTTGGCCATGTTGCCAGGCT 1977

QY 718 GGCCTTGAACTCCTGGCCTCAAAACAATCCACTTGCCTCGGCCTCCCAAGTGTATGATT 777

Db 1978 GGTCTTGAACTCCTGACATCAGGTGATCCACCTGGCCTCGGCCTCTAAAGTGTGGATT 2037

QY 778 ACAGGCGTGAGCCACCGTGCCTGGCCTAAACAATTAATTTATTTTATTTTATTTTAAATTT 2097

QY 838 GAAATTATACAATGAATTAATTTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGG 897

Db 2098 CAGCTTCTATTGAAATACAGGGGGCACATATATAGGAT--TGTTACATGGGTATATTGA 2155

QY 898 ACTTCTTCCCTCTATCTAACTGTATATTGTTACAGTTAACCAACCGTACTTCAATCCCA 957

Db 2156 ACTCAGGTAGTGATCATACTACCCACAGGTAGGTTTT---CAACCCACTCCCCCTCTT 2211

QY 958 CTCCTCTCTATCCTTCCCAACCTCTGATCACTCATTTCTACTCTCTACCTCCATGAGATC 1017

Db 2212 TTCCTCCCCATTCTAGTAGTGTGCAGTGCTATTGTTCTCATGTTTATGCTATGTGTGC 2271

QY 1018 CACTTTTTTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGC 1077

Db 2272 TCCAGGTTTAGCTCCCACTGTAAAGTGAGAACGTTGGTATTTGATTTTCTGTCCCTGTG 2331

QY 1078 TTATTTCACTTAACATAATGACTTCTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTT 1137

Db 2332 TTAATTCACCTTAGGATTATGGCTTCCAGCTCCCATTCATATTGCTGTAAGGATATGATTC 2391

QY 1138 CGTTCTTA 1145

Db 2392 ATTTTCA 2399

RESULT 4

US-09-151-376-3

; Sequence 3, Application US/09151376

; Patent No. 6676935

; GENERAL INFORMATION:

; APPLICANT: Henderson, D.R.

; APPLICANT: Schuur, E.R.

; TITLE OF INVENTION: TISSUE SPECIFIC VIRAL VECTORS

; FILE REFERENCE: 348022000221

; CURRENT APPLICATION NUMBER: US/09/151,376

; CURRENT FILING DATE: 1998-09-10

; EARLIER APPLICATION NUMBER: 08/669,753

; EARLIER FILING DATE: 1996-06-26

; EARLIER APPLICATION NUMBER: 08/495,034

; EARLIER FILING DATE: 1995-06-27

; NUMBER OF SEQ ID NOS: 71

; SOFTWARE: PatentIn Ver. 2.0

; SEQ ID NO 3

; LENGTH: 12047

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-151-376-3

Query Match 21.5%; Score 252.8; DB 4; Length 12047;

Best Local Similarity 64.2%; Pred. No. 3.1e-61;

Matches 429; Conservative 0; Mismatches 232; Indels 7; Gaps 3;

QY 478 AACTGGGATATCCATCACAATCAAAACATTTATTTTATTTTATGACAGAGTCTCACT 537

Db 1739 AAATGGTCTCCTCACTTTATTTATTTATTTATTTATTTAGATGGAGCCTCGCT 1798

QY 538 CTGTCAACCCAGGCTGGAGTGCAGTGGTGCCTACTCAGCTTACTGCAACCTCTGCCTGCCA 597

Db 1799 CTGTCTCCTAGGCTGGAGTGCATAGTGCATACCA-CTCACTGCAACCTCTGCCTCCTC 1857

QY 598 GGTTCAAAGCGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGATGCACCCAC 657

Db 1858 TGTTCAAAGTGATTTTCTTACCTCAGCCTCCCGAGTAGCTGGATTACAGGTGCGTGCCAC 1917

QY 658 AATGCCCAACTAATTTTGTATTTTGTAGTAGAGCGGGTTTGGCCATGTTGCCAGGCT 717

Db 1918 CACACCCGGCTAATTTTGTATTTTGTAGTAGAGCGGGTTTGGCCATGTTGCCAGGCT 1977

QY 718 GGCCTTGAACTCCTGGCCTCAAAACAATCCACTTGCCTCGGCCTCCCAAGTGTATGATT 777

Db 1978 GGTCTTGAACTCCTGACATCAGGTGATCCACCTGGCCTCGGCCTCTAAAGTGTGGATT 2037

QY 778 ACAGGCGTGAGCCACCGTGCCTGGCCTAAACAATTTATTTTCTTTTGTGTTGGGAATTT 837

Db 2038 ACAGGCGTGAGCCACCGTGCCTGGCCTAAACAATTTATTTTATTTTATTTTAAATTT 2097

QY 838 GAAATTATACAATGAATTAATTTGTTAACTGTCTATCTCCCTGCTGTGCTATGGAACACTGGG 897

Db 2098 CAGCTTCTATTGAAATACAGGGGGCACATATATAGGAT--TGTTACATGGGTATATTGA 2155

QY 898 ACTTCTTCCCTCTATCTAACTGTATATTGTTACAGTTAACCAACCGTACTTCAATCCCA 957

Db 2156 ACTCAGGTAGTGATCATACTACCCACAGGTAGGTTTT---CAACCCACTCCCCCTCTT 2211

QY 958 CTCCTCTCTATCCTTCCCAACCTCTGATCACTCATTTCTACTCTCTACCTCCATGAGATC 1017

Db 2212 TTCCTCCCCATTCTAGTAGTGTGCAGTGCTATTGTTCTCATGTTTATGCTATGTGTGC 2271

QY 1018 CACTTTTTTAGCTCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTCTGTGCCTGGC 1077

Db 2272 TCCAGGTTTAGCTCCCACTGTAAAGTGAGAACGTTGGTATTTGATTTTCTGTCCCTGTG 2331

QY 1078 TTATTTCACTTAACATAATGACTTCTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTT 1137

Db 1078 TTATTTCACTTAACATAATGACTTCTCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTT 1137

; CURRENT APPLICATION NUMBER: US/09/269,939A
; CURRENT FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: FR 97/10088
; PRIOR FILING DATE: 1997-08-06
; PRIOR APPLICATION NUMBER: FR 98/05032
; PRIOR FILING DATE: 1998-04-22
; NUMBER OF SEQ ID NOS: 41
; SOFTWARE: Patent.pm
; SEQ ID NO 19
; LENGTH: 22976
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: 1898..2253
; NAME/KEY: exon
; LOCATION: 3437..3781
; NAME/KEY: exon
; LOCATION: 12065..12184
; NAME/KEY: exon
; LOCATION: 15045..15101
; NAME/KEY: exon
; LOCATION: 15666..15812
; NAME/KEY: exon
; LOCATION: 19479..19652
; NAME/KEY: exon
; LOCATION: 19799..19858
; NAME/KEY: exon
; LOCATION: 19956..20087
; NAME/KEY: exon
; LOCATION: 20229..20854
; NAME/KEY: exon
; LOCATION: 20944..21094
; NAME/KEY: Misc Feature
; LOCATION: 19956..19958
; OTHER INFORMATION: Potential variant splicing site AAG
US-09-269-939A-19

Query Match		19.7%;	Score 232.4;	DB 4;	Length 22976;
Best Local Similarity		72.9%;	Pred. No. 2.8e-55;		
Matches 299;		Conservative	0;	Mismatches 111;	Indels 0; Gaps 0;
Qy	504	TTTTATTTT	TTATTTT	TATTTT	TAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGCAGTGG 563
Db	5787	TTTTTTTTT	TTTTTTT	TGACACAGAGTCTCACTCTGTGCCCCAGACTGCAGTACAGTGG 5728	
Qy	564	TGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCTCCAC 623			
Db	5727	TGGCATCTCAGCTCACTGCAACCTCTGCCTCTCGGTTCAAGCGATTCTCATGCTCAGC 5668			
Qy	624	CTCCCAAGTAGCTGGGACTACAGGCATGCACCAATGCCCAACTAATTTTGTATTTT 683			
Db	5667	CTCCTGAGTAGCTGGGATTACAGGCATGTGCCACCATGCTGCTAATCTTTGTATTTT 5608			
Qy	684	AGTAGAGACGGGGTTTGGCATGTTGCCAGGCTGGCCTTGAACCTCCTGGCCTCAAAACAA 743			
Db	5607	AGTAGAGACGGGGTTTCCACCATGTTGGCCAGGCTGCTGTGAACTCCTGACCTCAGGTGA 5548			
Qy	744	TCCACTTGCCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCC 803			
Db	5547	TCCACCCACCTTGGCCTCCCAAGTGTGAGATTACAGACGTGAGCCACCGTCCCCAGAC 5488			
Qy	804	TAAACATTATCTTTTCTTTGTGTTGGGAACCTTTGAAATTATACAATGAATTATTGTTAA 863			
Db	5487	TTTGAAATTCTCATACTCTTTCTTTATCTGCTTATTACTGCCAGTCTCACTCCACCAGA 5428			
Qy	864	CTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCTATC 913			
Db	5427	ATGTCATCTCCTTGACGACAGAACTTCAGCCATCCCAATCACCTCTATC 5378			

RESULT 8
US-09-499-522-1/c

; Sequence 1, Application US/09499522
; Patent No. 6479238
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Marta
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Bihain, Bernard
; TITLE OF INVENTION: POLYMORPHIC MARKERS OF THE LSR GENE
; FILE REFERENCE: GENSET.053AUS
; CURRENT APPLICATION NUMBER: US/09/499,522
; CURRENT FILING DATE: 2000-02-10
; EARLIER APPLICATION NUMBER: US 60/119,592
; EARLIER FILING DATE: 1999-02-10
; EARLIER APPLICATION NUMBER: US 60/144,784
; EARLIER FILING DATE: 1999-07-20
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: Patent.pm
; SEQ ID NO 1
; LENGTH: 23187
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: exon
; LOCATION: 2001..2356
; OTHER INFORMATION: exon1
; FEATURE:
; NAME/KEY: exon
; LOCATION: 3540..3884
; OTHER INFORMATION: exon2
; FEATURE:
; NAME/KEY: exon
; LOCATION: 12163..12282
; OTHER INFORMATION: exon3
; FEATURE:
; NAME/KEY: exon
; LOCATION: 15144..15200
; OTHER INFORMATION: exon4
; FEATURE:
; NAME/KEY: exon
; LOCATION: 15765..15911
; OTHER INFORMATION: exon5
; FEATURE:
; NAME/KEY: exon
; LOCATION: 19579..19752
; OTHER INFORMATION: exon6
; FEATURE:
; NAME/KEY: exon
; LOCATION: 19899..19958
; OTHER INFORMATION: exon7
; FEATURE:
; NAME/KEY: exon
; LOCATION: 20056..20187
; OTHER INFORMATION: exon8
; FEATURE:
; NAME/KEY: exon
; LOCATION: 20329..20957
; OTHER INFORMATION: exon9
; FEATURE:
; NAME/KEY: exon
; LOCATION: 21047..21187
; OTHER INFORMATION: exon10
; FEATURE:
; NAME/KEY: polyA signal
; LOCATION: 21168..21173
; OTHER INFORMATION: AATAAA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..2000
; OTHER INFORMATION: potential 5'regulatory region
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 22324..23187
; OTHER INFORMATION: homology with USF2 gene in ref: embl Y07661
; FEATURE:

Db 5711 AGTAGAGACGGGTTTCCACCATGTTGGCCAGGCTGGTCTGGAACCTCCTGACCTCAGGTGA 5652
Qy 744 TCCACTTGCCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCCTGGCC 803
Db 5651 TCCACCCACCTTGGCTCCCAAGTGTCTGAGATTACAGACGTTGAGCCACCGTGCCCGAC 5592
Qy 804 TAAACATTTATCTTTCTTGTGTTGGGAACCTTGAATTTATACAAATGATTTATTGTTAA 863
Db 5591 TTTGAAATTTCTCATACTCTTTCTTTATCTGCTTATTACTGCCAGTCTCACTCCACCAGA 5532
Qy 864 CTGTCATCTCCCTGCTGCTGCTATGGAACACTGGGACTTCTTCCCTCTATC 913
Db 5531 ATGTCATCTCCTTGACGACAGAAACTTTCAGCCATCCCAATCACCTCTATC 5482

RESULT 9

US-09-798-096-10/c
; Sequence 10, Application US/09798096
; Patent No. 639378
; GENERAL INFORMATION:
; APPLICANT: Donna T. Ward
; APPLICANT: Andrew T. Watt
; TITLE OF INVENTION: ANTISENSE MODULATION OF REQL2 EXPRESSION
; FILE REFERENCE: RTS-0207
; CURRENT APPLICATION NUMBER: US/09/798,096
; CURRENT FILING DATE: 2001-03-01
; NUMBER OF SEQ ID NOS: 89
; SEQ ID NO 10
; LENGTH: 99500
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
US-09-798-096-10

Query Match 19.6%; Score 231.2; DB 4; Length 99500;
Best Local Similarity 78.1%; Pred. No. 1.4e-54;
Matches 278; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
Qy 504 TTTATTTTATTTTATTTTATGACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGG 563
Db 66170 TTGTTTGTGTTTGTGTTGAGACAGAGTCTCACTCTGTGCCCCAGGCTGGAGTGCAGTGG 66111
Qy 564 TGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCCCTCCAC 623
Db 66110 CACAATCTTGGCTCACTACAACTCTGCTGCTGGTTCAAGCCATTCTCTGCTCAGC 66051
Qy 624 CTCCCAAGTAGCTGGGACTACAGGCATGCAACCAATGCCCAACTAATTTTGTATTTT 683
Db 66050 CTCCCAAGTAGCTGGGATTATGATGCCCAACCATCGGCCAGCTAATTTTGTATTTT 65991
Qy 684 AGTAGAGACGGGTTTGGCCATGTTGCCAGGCTGGCCTTGAACCTCGCCCTCAACAA 743
Db 65990 AGTAGAGACAGAGTTTACCATGTTGGCCAGGCTGCTCGAATCTCGAATCTCGACCTCAAGCAA 65931
Qy 744 TCCACTTGCCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCCTGGCC 803
Db 65930 TCCACTTGCCCTTGCCCTCCCAAGTGTGCTGGGATTACAGGCATGAGCCACCGGCCAGCC 65871
Qy 804 TAAACATTTATCTTTTCTTGTGTTGGGAATTTGAAATTTATACAAATGATTTATTG 859
Db 65870 TACCAAGTAGCTTTAAGTTGAATATTGTCGCTAGCAGCTTACACAATAGAACACTG 65815

RESULT 10

US-08-724-394A-20
; Sequence 20, Application US/08724394A
; Patent No. 587237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston

; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237e1
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 20:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cdna
; FEATURE:
; NAME/KEY: misc.feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note="HLA-H.CONTIG"
US-08-724-394A-20

Query Match 19.5%; Score 229.2; DB 2; Length 246240;
Best Local Similarity 75.4%; Pred. No. 8.5e-54;
Matches 285; Conservative 0; Mismatches 93; Indels 0; Gaps 0;
Qy 426 TACATGTGATATTGGATACATGATATACAAATATATATATATATATATATATATATAT 485
Db 85558 TAAACATGAATTCACATAATATAGTAGTACATTTATGTTTAAATTTGTTTATCTTTT 85617
Qy 486 TATCCATCACATCAAAACATTTATTTTATTTCTTTTATAGACAGAGTCTCACTCTGTCA 545
Db 85618 GGTGACTCCTTTCATCTCTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 85677
Qy 546 CAGGCTGGAGTGCAGTGGTGGCTCATCTCAGCTTACTGCAACCTCTGCCCTGCCAGTTCA 605
Db 85678 CAGGCTGATGTAGTGGCGAAATCTCAGCTCACTGCAACCTCTGCCCTGCCCGTTCA 85737
Qy 606 CGATTCTCATGCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCAATGCCCA 665
Db 85738 TGATTCTGTGCTTCAGCCCTCCCAAGTAGCTGGGATTACAGGCATGTGCCCAATGCC 85797
Qy 666 ACTAATTTTGTATTTTGTAGTAGAGACGGGTTTGGCATGTTGCCAGGCTGGCTTGA 725
Db 85798 GCTAATTTGTATTTTGTAGTAGAGCCAGGTTTGGCATGTTGGCAGGCTGGCTTGA 85857
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Db 85918 GAGCCACCGTGCCTGGCC 85935

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RESULT 11
US-08-724-394A-21
; Sequence 21, Application US/08724394A
; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
; INFORMATION FOR SEQ ID NO: 21:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 246240 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: not relevant
; TOPOLOGY: not relevant
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: 1..246240
; OTHER INFORMATION: /note= "HLA-H.CONTIG"
US-08-724-394A-21

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QY	786	GAGCCACCGTGCCTGGCC	803
Db	85918	GAGCCACCACACCTGGCC	85935

RESULT 12
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; Patent No. 5872237
; GENERAL INFORMATION:
; APPLICANT: Feder, John N.
; APPLICANT: Kronmal, Gregory S.
; APPLICANT: Lauer, Peter M.
; APPLICANT: Ruddy, David A.
; APPLICANT: Thomas, Winston
; APPLICANT: Tsuchihashi, Zenta
; APPLICANT: Wolff, Roger K.
; TITLE OF INVENTION: Megabase Transcript Map: No. 5872237el
; TITLE OF INVENTION: Sequences and Antibodies Thereto
; NUMBER OF SEQUENCES: 31
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: TOWNSEND and TOWNSEND and CREW LLP
; STREET: Two Embarcadero Center, 8th Floor
; CITY: San Francisco
; STATE: CA
; COUNTRY: USA
; ZIP: 94111-3834
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/724,394A
; FILING DATE: 01-OCT-1996
; CLASSIFICATION: 536
; ATTORNEY/AGENT INFORMATION:
; NAME: Fitts, Renee A.
; REGISTRATION NUMBER: 35,136
; REFERENCE/DOCKET NUMBER: 017957-000100
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-576-0200
; TELEFAX: 415-576-0300
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; TOPOLOGY: not relevant
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US-08-724-394A-22

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; PRIOR APPLICATION NUMBER: FR 98/05032
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; NAME/KEY: Misc_Feature
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

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(without alignments)
2501.860 Million cell updates/sec

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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 3470272 seqs, 21671516995 residues
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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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4	596	100.0	1177	6	AX362451	AX362451 Sequence
5	596	100.0	1177	6	AX376314	AX376314 Sequence
6	596	100.0	1177	6	AX454686	AX454686 Sequence
7	596	100.0	1177	6	AX491164	AX491164 Sequence
8	596	100.0	1177	9	AY358613	AY358613 Homo sapi
9	596	100.0	3566	9	AK127751	AK127751 Homo sapi
10	596	100.0	159272	9	HSDJ686C3	AL049712 Human DNA
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14	221	37.1	259335	2	AC130173	AC130173 Rattus no
15	165.5	27.8	3216	10	AF417581	AF417581 Mus muscu
16	162.5	27.3	3169	9	AF417580	AF417580 Homo sapi
17	159	26.7	189755	2	BX571945	BX571945 Danio rer
18	152.5	25.6	148762	2	BX322786	BX322786 Danio rer
19	152.5	25.6	177584	2	BX296526	BX296526 Danio rer
20	151	25.3	1977	5	AY263168	AY263168 Takifugu
21	144	24.2	2871	5	AY263167	AY263167 Takifugu
22	137	23.0	214504	10	AC102779	AC102779 Mus muscu
23	137	23.0	242249	10	AC102790	AC102790 Mus muscu
24	137	23.0	340350	2	AC112299	AC112299 Rattus no
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27	131	22.0	2895	10	AF417579	AF417579 Mus muscu
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30	102	17.1	242241	2	AC111252	AC111252 Rattus no
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32	95	15.9	124950	9	AC108059	AC108059 Homo sapi
33	94.5	15.9	1749	5	AY263172	AY263172 Takifugu
34	94	15.8	2572	3	AY263175	AY263175 Anopheles
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ALIGNMENTS

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Baker,K.P., Desnovers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0193983-A 211 13-DEC-2001;
Genentech Inc. (US)
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QY 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
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DEFINITION Sequence 211 from Patent WO0208288.
ACCESSION AX362451
VERSION AX362451.1 GI:18694683
KEYWORDS
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
REFERENCE 1
AUTHORS Baker,K.P., Desnovers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
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JOURNAL Patent: WO 0208288-A 211 31-JAN-2002;
Genentech, Inc. (US)
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AX376314
LOCUS AX376314 1177 bp DNA linear PAT 01-MAR-2002
DEFINITION Sequence 381 from Patent WO0168848.
ACCESSION AX376314
VERSION AX376314.1 GI:19170548
KEYWORDS
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ORGANISM Homo sapiens (human)
Homo sapiens
REFERENCE 1
AUTHORS Baker,K.P., Chen,J., Desnovers,L., Goddard,A., Godowski,P.J.,
Gurney,A.L., Pan,J., Smith,V., Watanabe,C.K., Wood,W.I. and
Zhang,Z.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0168848-A 381 20-SEP-2001;
Genentech, Inc. (US)
FEATURES Location/Qualifiers
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Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-10-063-736-130 (1-111) x AX362451 (1-1177)
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Db 10 ATGGGCTCCTGCTGCTGGTGTCTTCTCCTCAGCCCTCGCGGTGGCCTACACCATCATG 69
QY 21 SerLeuProProSerPheAspCysGlyProPheArgCysArgValSerValAlaArgGlu 40
Db 70 TCCCTCCACCCCTCCTTTGACTGGGCGGCTTACAGTGAGTCTCAGTTGCCCGGGAG 129
QY 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
Db 130 CACCTCCACCCCTCCTTTGACTGGGCGGCTTACAGTGAGTCTCAGTTGCCCGGGAG 129
QY 61 SerCysGlnProValLysGlyHisGlyThrLeuGlyGluSerProMetProPheLysArg 80
Db 190 TCATGCCAGCCTGTAAAGGCCCATGGAACCTTTGGTGGAATCACCGATGCCATTAAAGAGG 249
QY 81 ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSerSer 100
Db 250 GTTTTCTGCCAGGATGGAATGTTAGGTGCTTCTGTCTGCGCTGTTTCATTTCAGTAGC 309
QY 101 HisGlnProProValAlaValGluCysLeuLys 111
Db 310 CACCAGCCACCTGTGGCGGTGAGTGCTTGAAA 342

SRSNFFYMGLLLLLVLFLSLLPVAYTMSLPPSPDCGPFRCRVSVAREHLP SRGSLLRG
PRPRIPLVLSVCQPKVKGHTLGESPMFPRVFCQDGNVRSFCVAVHFSHQPPVAVEC
Lk¹¹

ORIGIN

Alignment Scores:		
pred. No.:	7.33e-43	3566
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DB:	9	0
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	Matches:	
	Conservative:	
	Mismatches:	
	Indels:	
	Gaps:	

US-10-063-736-130 (1-111) X AK127751 (1-3566)

Qy	1	MetGlyLeuLeuLeuValLeuPheLeuSerLeuLeuProValAlaTyrThrIleMet	20
Db	376	ATGGGCTCCTGCTGCTGGTGTCTTCTCAGGCTCCTGCGGTGGCCTACACCATCATG	435
Qy	21	SerLeuProProSerPheAspCysGlyPropheArgCysArgValSerValAlaArgGlu	40
Db	436	TCCCTCCCACCCCTCCTTTGACTCGGGCCGTTCAGGTGCAGAGTCTCAGTTGCCCGGAG	495
Qy	41	HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal	60
Db	496	CACCTCCCTCCCGAGGCAGTCTGCTCAGAGGGCCCTCGGCCCAGAAATCCAGTTCGTGTT	555
Qy	61	SerCysGlnProValLysGlyHisGlyThrLeuGlyGluSerProMetProPheLysArg	80
Db	556	TCATGCCAGCCTGTAAAGGCCATGGAACTTTGGTGTGAATCACCGATGCCATTTAAGAGG	615
Qy	81	ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSerSer	100
Db	616	GTTTCTGCCAGGATGGAAATGTAGGTGTTCTGTGTCTGCGCTGTTTCATTTCAGTAGC	675
Qy	101	HisGlnProProValAlaValGluCysLeuLys	111
Db	676	CACAGCCACCTGTGGCCGTTGAGTGTCTTGAAA	708

RESULT 10

HSDJ686C3/c	HSDJ686C3	159272 bp	DNA linear	PRI 14-FEB-2001
LOCUS	Human DNA sequence from clone RP4-686C3 on chromosome 20. Contains			
DEFINITION	the IDH3B gene for isocitrate dehydrogenase 3 (NAD+) beta A and B, the gene for nucleolar protein NOP56, a novel gene, ESTs, STSS, GSSs and three CpG islands, complete sequence.			

chromosome 20, constructed by the Sanger Centre Chromosome 20 Mapping Group. Further information can be found at <http://www.sanger.ac.uk/HGP/Chr20>. This sequence is the entire insert of clone RP4-686C3. This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality ≥ 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest. RP4-686C3 is from the library RPCI-4 constructed by the group of Pieter de Jong. For further details see

FEATURES source

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Location/Qualifiers
1. .159272
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="20"
/clone="RP4-686C3"
/clone_lib="RPCI-4"
1. .239
/note="AluX repeat: matches 59. .297 of consensus"
641. .866
/note="MLT1J repeat: matches 163. .403 of consensus"
886. .1010
/note="AluJb repeat: matches 2. .133 of consensus"
1152. .1314
/note="MER5B repeat: matches 1. .166 of consensus"
1358. .1406
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1576. .1671
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1817. .2022
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2106. .2359
/note="AluX repeat: matches 1. .291 of consensus"
2561. .2586
/note="13 copies 2 mer tg 96% conserved"
2912. .3121
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3666. .3892
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4086. .4169
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4170. .4466
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4467. .4502
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4738. .5055
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/note="AluX repeat: matches 1. .221 of consensus"
6340. .6510
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6588. .6883
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6896. .7095
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12156. .12250,12364. .12424,13112. .13554)
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beta (isoform C))"
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match: ESTs: Em:AUI36511"

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11773..11919,12156..12250,12364..12424,13112..13554)
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beta (isoform B))"
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Em:AA800287 Em:AI171432 Em:AI171793 Em:AA306790
Em:AA144481 Em:AA189176 Em:AA153798 Em:AI105469
Em:AA980536 Em:AA268842 Em:AI566177 Em:R15323 Em:AA062738
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11773..11919,12156..12250,12364..12424,13427..13554)
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beta (isoform A))"
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VIIREQTEGEYSSLEHESARGVIECLKIVTRAKSORIAKFAFDYATKKGRGKVTAVHK
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8972..9274
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10738..10773
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12364..12424,13112..13198)
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CDS
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Pred. No.: 3.34e-41 Length: 159272
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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US-10-063-736-130 (1-111) x HSDJ686C3 (1-159272)
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QY 21 SerLeuProProSerPheAspCysGlyProPheArgCysArgValSerValAlaArgGlu 40
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RESULT 11
AX833218
LOCUS AX833218 2560 bp DNA linear PAT 15-DEC-2003
DEFINITION Sequence 342 from Patent EPL347046.
ACCESSION AX833218
VERSION AX833218.1 GI:39919353
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S.,
Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R.,
Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and
Masuho,Y.

TITLE Full-length cDNA sequences
JOURNAL Patent: EP 1347046-A 342 24-SEP-2003;
Research Association for Biotechnology (JP)
FEATURES Location/Qualifiers

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1. .2560
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Best Local Similarity: 97.99% Indels: 0
Query Match: 6 Gaps: 0
DB:

US-10-063-736-130 (1-111) x AX833218 (1-2560)

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QY 21 SerLeuProProSerPheAspCysGlyProPheArgCysArgValSerValAlaArgGlu 40
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QY 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
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RESULT 12

AK094789
LOCUS AK094789 2560 bp mRNA linear PRI 15-JUL-2002
DEFINITION Homo sapiens cDNA FLJ37470 fis, clone BRAWH2012258.
ACCESSION AK094789
VERSION AK094789.1 GI:21753918
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T.,
Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R.,
Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H.,
Onogawa, S., Kaeriyama, S., Satch, N., Matsunawa, H., Takahashi, E.,
Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S.,
Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T.,
Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y.,
Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H.,
Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K.,
Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A.,
Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S.,
Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.

NEDO human cDNA sequencing project

Unpublished

2 (bases 1 to 2560)

Isogai, T. and Yamamoto, J.

Direct Submission

TITLE

JOURNAL

REFERENCE

AUTHORS

TITLE

JOURNAL

Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:
Research Association for Biotechnology (RAB); cDNA library
construction: Helix Research Institute (HRI) (supported by Japan
Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB,
HRI, and Biotechnology Center, National Institute of Technology and
Evaluation; clone selection for full insert sequencing: HRI and
RAB; annotation: HRI and RAB.

FEATURES

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CDS

ORIGIN

Alignment Scores: 5.95e-42 Length: 2560
Pred. No.: 584.00 Matches: 109
Score: 99.10% Conservative: 1
Percent Similarity: 98.20% Mismatches: 1
Best Local Similarity: 97.99% Indels: 0
Query Match: 6 Gaps: 0
DB:

US-10-063-736-130 (1-111) x AK094789 (1-2560)

QY 1 MetGlyLeuLeuLeuValLeuPheLeuSerLeuLeuProValAlaTyrThrIleMet 20
Db ATGGGCTCTCTGCTGCTGCTGCTTCTCTCAGCCTCCTGCGGTGGCTACACCATCATG 1566
QY 21 SerLeuProProSerPheAspCysGlyProPheArgCysArgValSerValAlaArgGlu 40
Db TCCCTCCACCTCTCTTGTACTGCGGCCGTTTCAGGTGCAGAGTCTCAGTTGCCAGGAG 1626
QY 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60
Db CACCTCCCTCCCGAGGAGTCTGCTCAGAGGGCCTTGGCCAGAAATTCAGTTCTGGTT 1686
QY 61 SerCysGlnProValLysGlyHisGlyThrLeuGlyGluSerProMetProPheLysArg 80
Db TCATGCCAGCCTGTAAAGGCCATGGAACTTTGGGTGAATCACCGATGCCATTAAAGAGG 1746
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QY 101 HisGlnProProValAlaValGluCysLeuLys 111
Db CACCAGCCACCTGTGGCCGTTGAGTCTTGAA 1839

RESULT 13

AL833804

LOCUS

DEFINITION

Mouse DNA sequence from clone RP23-20A6 on chromosome 2, complete

ACCESSION

VERSION

KEYWORDS

200521 bp DNA linear ROD 24-JUN-2003

AL833804

GI:32187965

HTG.

SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 200521)
Griffiths,C.
Direct Submission
Submitted (24-JUN-2003) Wellcome Trust Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk
On Jun 24, 2003 this sequence version replaced gi:32131092.
Sequence from the Mouse Genome Sequencing Consortium whole genome shotgun may have been used to confirm this sequence. Sequence data from the whole genome shotgun alone has only been used where it has a phred quality of at least 30.
----- Genome Center
Center: Wellcome Trust Sanger Institute
Center code: SC
Web site: <http://www.sanger.ac.uk>
Contact: humquery@sanger.ac.uk

During sequence assembly data is compared from overlapping clones. Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.
This sequence was finished as follows unless otherwise noted: all regions were either double-stranded or sequenced with an alternate chemistry or covered by high quality data (i.e., phred quality >= 30); an attempt was made to resolve all sequencing problems, such as compressions and repeats; all regions were covered by at least one plasmid subclone or more than one M13 subclone; and the assembly was confirmed by restriction digest, except on the rare occasion of the clone being a YAC.
The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases: Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep RP23-20A6 is from the RPCI-23 Mouse BAC Library
constructed by the group of Pieter de Jong.
For further details see <http://www.chori.org/bacpac/home.htm>
VECTOR: pBACE3.6.
FEATURES
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Best Local Similarity: 54.05% Mismatches: 27
Query Match: 38.09% Indels: 17
DB: 10 Gaps: 4
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Db 159026 TCTCTCCACCCCTCGTTTGACTGTGGCCCTTCAGGTGTGCTCTTTGTTGCTGGGGACAG 159085
QY 41 HisLeuProSerArgGlySerLeuLeuArgGlyProArgProArgIleProValLeuVal 60

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QY 61 SerCysGlnProValLysGlyHisGlyThrLeuGlyGluSerProMetProPheLysArg 80
Db 159122 TCATGCCAGCCTGTGAGAGGCTCTGGGGCTTTAGGGGAACCACTAAACCATCCAGTAA- 159180
QY 81 ValPheCysGlnAspGlyAsnValArgSerPheCysValCysAlaValHisPheSerSer 100
Db 159181 GTTTTCTGTAAGGAGGGAGAT-----GCCCATGT-----GGTAGC 159216
QY 101 HisGlnProProValAlaValGluCysLeuLys 111
Db 159217 AGGCAGCTACTTGTGGCTATGGAATTCATAAA 159249

RESULT 14
AC130173/c
LOCUS AC130173.6 GI:30522576 259335 bp DNA linear HTG 10-MAY-2003
DEFINITION Rattus norvegicus clone CH230-11D24, *** SEQUENCING IN PROGRESS
KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS_ENRICHED.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 259335)
AUTHORS Muzny,D.,Marie., Metzker,M.Lee., Abramzon,S., Adams,C., Alder,J., Allen,C., Allen,H., Alsbrooks,S., Amin,A., Anguiano,D., Anyalebechi,V., Aoyagi,A., Ayodeji,M., Baca,E., Baden,H., Baldwin,D., Bandaranaike,D., Barber,M., Barnstead,M., Benahmed,F., Biswal,K., Blair,J., Blankenburg,K., Blyth,P., Brown,M., Bryant,N., Buhay,C., Burch,P., Burrell,K., Calderon,E., Cardenas,V., Carter,K., Cavazos,I., Ceasar,H., Chen,A., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Y., Chen,Z., Chu,J., Cleveland,C., Cockrell,R., Cox,C., Coyle,M., Cree,A., D'Souza,L., Davila,M.L., Davis,C., Davy-Carroll,L., De Anda,C., Dederich,D., Delgado,O., Denson,S., Deramo,C., Ding,Y., Dinh,H., Divya,K., Draper,H., Dugan-Rocha,S., Dunn,A., Durbin,K., Duval,B., Eaves,K., Egan,A., Escotto,M., Eugene,C., Evans,C.A., Falls,T., Fan,G., Fernandez,S., Finley,M., Flagg,N., Forbes,L., Foster,M., Foster,P., Fraser,C.M., Gabisi,A., Ganta,R., Garcia,A., Garner,T., Garza,M., Gebregeorgis,E., Geer,K., Gill,R., Grady,M., Guerra,W., Guevara,W., Gunaratne,P., Haaland,W., Hamil,C., Hamilton,C., Hamilton,K., Harvey,Y., Havlak,P., Hawes,A., Henderson,N., Hernandez,J., Hernandez,R., Hines,S., Hladun,S.L., Hodgson,A., Hognes,M., Hollins,B., Howells,S., Hulyk,S., Hume,J., Idlebird,D., Jackson,A., Jackson,L., Jacob,L., Jiang,H., Johnson,B., Johnson,R., Jolivet,A., Karpathy,S., Kelly,S., Kelly,S., Khan,Z., King,L., Kovar,C., Kowis,C., Kraft,C.L., Lebow,H., Levan,J., Lewis,L., Li,Z., Liu,J., Liu,J., Liu,W., Liu,Y., London,P., Longacre,S., Lopez,J., Lorensuhewa,L., Loulseged,H., Lozado,R.J., Lu,X., Ma,J., Maheshwari,M., Mahindartne,M., Mahmud,M., Malloy,K., Mangum,A., Mangum,B., Mapua,P., Martin,K., Martin,R., Martinez,E., Mawhiney,S., McLeod,M.P., McNeill,T.Z., Meenen,E., Milosavljevic,A., Miner,G., Minja,E., Montemayor,J., Moore,S., Morgan,M., Morris,K., Morris,S., Munidasa,M., Murphy,M., Nair,L., Nankervis,C., Neal,D., Newton,N., Nguyen,N., Norris,S., Nwaokemeleh,O., Okwuonu,G., Olarnpunsagoon,A., Pal,S., Parks,K., Pasternak,S., Paul,H., Perez,A., Perez,L., Pfannkoch,C., Plopper,F., Poindexter,A., Popovic,D., Primus,E., Pu,L.-L., Puazo,M., Quiroz,J., Rachlin,E., Reeves,K., Regier,M.A., Reigh,R., Reilly,B., Reilly,M., Ren,Y., Reuter,M., Richards,S., Riggs,F., Rives,C., Rodkey,T., Rojas,A., Rose,M., Rose,R., Ruiz,S.J., Sanders,W., Savery,G., Scherer,S., Scott,G., Shatsman,S., Shen,H., Shetty,J., Shvartsbeyn,A., Sisson,I., Sitter,C.D., Smajs,D., Sneed,A., Sodergren,E., Song,X.-Z., Sorelle,R., Sosa,J., Steimle,M., Strong,R., Sutton,A., Svatek,A., Tabor,P., Taylor,C., Taylor,T., Thomas,N., Thomas,S., Tingey,A., Trejos,Z., Usmani,K., Valas,R., Vera,V., Villasana,D., Waldron,L., Walker,B., Wang,J., Wang,Q., Wang,S., Warren,J., Warren,R., Wei,X., White,F.,

ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 3216)
AUTHORS Kurima,K., Peters,L.M., Yang,Y., Riazuddin,S., Ahmed,Z.M., Naz,S.,
Arnaud,D., Drury,S., Mo,J., Makishima,T., Ghosh,M., Menon,P.S.N.,
Deshmukh,D., Oddoux,C., Ostrer,H., Khan,S., Raizuddin,S.,
Deininger,P.L., Hampton,L.L., Sullivan,S.L., Battey,J.F.,
Keats,B.J.B., Wilcox,E.R., Friedman,T.B. and Griffith,A.J.
TITLE Dominant and recessive deafness caused by mutations of a novel
gene, TMCL, required for cochlear hair-cell function
Nat. Genet. 30 (3), 277-284 (2002)

JOURNAL 21918583
MEDLINE 11850618
PUBMED
REFERENCE 2 (bases 1 to 3216)
AUTHORS Kurima,K., Griffith,A.J. and Friedman,T.B.
TITLE Direct Submission
JOURNAL Submitted (10-SEP-2001) NIDCD, NIH, 5 Research Court, #2A02,
Rockville, MD 20850, USA

FEATURES
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/chromosome="2"

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322..2988
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ORIGIN

Alignment Scores:
Pred. No.: 4.23e-05 Length: 3216
Score: 165.50 Matches: 49
Percent Similarity: 51.92% Conservative: 5
Best Local Similarity: 47.12% Mismatches: 13
Query Match: 27.77% Indels: 37
DB: 10 Gaps: 5

US-10-063-736-130 (1-111) x AF417581 (1-3216)

QY 1 MetGlyLeuLeuLeuValLeuPheLeuSerLeuLeuProValAlaTyrThrIleMet 20
Db 2353 ATGGGCCTGCTGCTGTTGGTGCTCTCTTCCTCAGCCTCCTGCCTGTGGCCTACACCGTCATG 2412
QY 21 SerLeuProProSerPheAspCysGlyProPhe-----Arg-CysArgValse 36
Db 2413 TCTCTCCACCCCTCGTTTGACTGTGGCCCTTCAGTGGGAAAAACAGATGTACGATGTC 2472
QY 36 rValAlaArgGluHisLeuProSerArgGlySerLeuLeuArgGlyPro-ArgProArgI 56
Db 2473 CTCCATGAGA-----CCATCGAGACGAT 2496

QY 56 lePro-----ValLeuValSerCysGlnPro----- 64
Db 2497 TTCCCTAAGTTCTCTGGGCAAGATCTTTGCGTTTCCTTGCCCAACCCAGGCCTGATCATTCCTCA 2556
QY 65 -----VallYsGlyHisGlyThrLeuGlyGluSerProMetProPheLysA 80
Db 2557 GCCATCCTGCTAATGTTTCTGGCCATTACTA-----TCTGAACTCAGTTTTCAAAA 2607
QY 80 rgValPhe 82
Db 2608 AGTCTTTC 2615

Search completed: September 17, 2004, 00:01:03
Job time : 2008 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 18:36:54 ; Search time 2916 Seconds
(without alignments)
12053.425 Million cell updates/sec

Title: US-10-063-736-129
Perfect score: 1177
Sequence: 1 aacttctacatggcctoct.....ataaccacacatggcaaaa 1177

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues
Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : EST:*

- 1: em_estba:*
- 2: em_esthum:*
- 3: em_estin:*
- 4: em_estmu:*
- 5: em_estov:*
- 6: em_estpl:*
- 7: em_estro:*
- 8: em_htc:*
- 9: gb_est1:*
- 10: gb_est2:*
- 11: gb_htc:*
- 12: gb_est3:*
- 13: gb_est4:*
- 14: gb_est5:*
- 15: em_estfun:*
- 16: em_estom:*
- 17: em_gss_hum:*
- 18: em_gss_inv:*
- 19: em_gss_pln:*
- 20: em_gss_vrt:*
- 21: em_gss_fun:*
- 22: em_gss_mam:*
- 23: em_gss_mus:*
- 24: em_gss_pro:*
- 25: em_gss_rod:*
- 26: em_gss_phg:*
- 27: em_gss_vrl:*
- 28: gb_gss1:*
- 29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	430.6	36.6	472	AQ203589	AQ203589 HS_3103_B
2	353.6	30.0	376	AQ139929	AQ139929 HS_3104_A
3	305	25.9	653	BM565530	BM565530 ih26d08.x
4	244	20.7	1201	BX382054	BX382054 BX382054

/mol_type="genomic DNA"
 /db_xref="taxon:9606"
 /clone="Plate=3104 Col=20 Row=G"
 /sex="male"
 /clone_lib="CIT Approved Human Genomic Sperm Library D"
 /note="Organ: sperm; Vector: pBelOBAC11; BAC Clones in E-Coli DH10B"

ORIGIN

Query Match 30.0%; Score 353.6; DB 28; Length 376;
 Best Local Similarity 96.3%; Pred. No. 1.2e-62;
 Matches 362; Conservative 0; Mismatches 14; Indels 0; Gaps 0;

QY 263 ATGGAATGTTAGGTCGTTCTGTCTCGCTGTTTCATTTTCAGTAGCCACGACCTG 322
 Db |||||
 1 ATGGAATGTTAGGTCGTTCTGTCTCGCTGTTTCATTTTCAGTAGCCACGACCTG 60
 QY 323 TGGCCGTTGAGTCTGAAATGAGGAACCTGAGAAAATTAATTTCTCATGTATTTTCTCA 382
 Db |||||
 61 TGGCCGTTGAGTCTGAAATGAGGAACCTGAGAAAATTAATTTCTCATGTATTTTCTCA 120
 QY 383 TTTATTATTAAATTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTGGA 442
 Db |||||
 121 TTTATTATTAAATTTTAACTGATAGTTGTACATATTTGGGGGTACATGTGATATTGGA 180
 QY 443 TACATGTATACAATATATAATCATCAAAATCAGGGTAAGTGGGATATCCATCATCAAAC 502
 Db |||||
 181 TACATGTATACAATATATAATCATCAAAATCAGGGTAAGTGGGATATCCATCATCAAAC 240
 QY 503 ATTTATTTTATTTCTTTTATGACAGAGTCTCACTGTCTCACCAGGCTGGAGTGCAGTG 562
 Db |||||
 241 ATTTATTTTATTTCTTTTATGACAGAGTCTCACTGTCTCACCAGGCTGGAGTGCAGTG 300
 QY 563 GTGCCATCTCAGCTTACTGCAACCTCTGCCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCA 622
 Db |||||
 301 GTGCCATCTCAGCTTACTGCAACCTCTGCCCTGCCAGGTTAAGCGATTCTCATGCCCTTCA 360
 QY 623 CTTCCCAAGTAGCTGG 638
 Db |||||
 361 TCTCTCAAGATTCTTG 376

RESULT 3
 BM565530
 LOCUS BM565530 653 bp mRNA linear EST 20-FEB-2002
 DEFINITION ih26d08.x1 Human insulinoma Homo sapiens cDNA 3', mRNA sequence.
 ACCESSION BM565530
 VERSION BM565530.1 GI:18825776
 KEYWORDS EST.
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 653)
 AUTHORS Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K., Lemishka,I., Searce,M., Brestelli,J., Gradwohl,G., Clifton,S., Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and Bowers,Y.
 TITLE Endocrine Pancreas Consortium
 JOURNAL Unpublished (2000)
 COMMENT Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
 Endocrine Pancreas Consortium
 Harvard University, Howard Hughes Medical Institute
 Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge, MA 02138
 Tel: 617-495-1812
 Fax: 617-495-8557
 Email: dmelton@biohp.harvard.edu
 Library was constructed by Dr. J. Ferrer In vivo mass-excised to pBluescript SK- by Dr. H. Inoue DNA sequencing by: Washington University Genome Sequencing Center For information on obtaining a

clone please contact: Dr. Hiroshi Inoue (hinoue@im.wustl.edu)
 Seq primer: -40UP from Gibco
 High quality sequence stop: 476.
 FEATURES
 source Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
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 /clone_lib="Human insulinoma"
 /note="Organ: pancreas; Vector: pBluescript SK-; Site 1: XhoI; Site 2: EcoRI; Constructed with lambda ZAPII system (Stratagene) by Dr. J. Ferrer, in vivo mass-excised to pBluescript SK- by Dr. H. Inoue following the Washington University protocol
 (http://genome.wustl.edu/est/lambda_protocol.shtml).
 Please contact Hiroshi Inoue, MD/PhD for further information on this library (Metabolism Division, Permutt Laboratory, Washington University School of Medicine, Box 8127, 660 S Euclid Ave, St. Louis, MO 63110). Note: this is a Washington University Pancreas EST project library."

ORIGIN

Query Match 25.9%; Score 305; DB 12; Length 653;
 Best Local Similarity 73.4%; Pred. No. 1.2e-52;
 Matches 481; Conservative 0; Mismatches 145; Indels 29; Gaps 6;

QY 508 TTTTATTATCTTTTATGACAGAGTCTCACTC-TGTACCCAGGCTGGAGTGCAGTGGTGC 566
 Db |||||
 2 TTTTATTATCTTTTATGACAGAGTTCACCTCTTGTGCCCAGGCTGGAGTGTAAATGGGT 61
 QY 567 CATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACCTC 626
 Db |||||
 62 GATCTCGGCTCACCACAACCTCTGCCTCCAGGTTCAACAAATTC--TGCCTCAGCTC 118
 QY 627 CCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTGTATTTTAGT 686
 Db |||||
 119 CCAAGTAGCTGGGATTACAGGCATGCACCACCACGCTGGCTAATTTT---GTTTAGT 174
 QY 687 AGAGACGGGGTTTGGCCATGTTGCCAGGCTGGCCCTGAACTCCTGGCCCTCAACAATCC 746
 Db |||||
 175 AGAGACAGGGTTTCTCCATGTTGGTCAGGCTGGTCTCAAACTCCCGACCTCAGGTGATCC 234
 QY 747 ACTTGCCTCGGCCCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCCT-- 804
 Db |||||
 235 GCCCACCCTGGCCTCCCAAGTGTGGGATTACAGGCAATGAGCCACCACGCCCCACCTTG 294
 QY 805 -----AAACATTTATCTTTTCTTTGTGTGGGAACCTTTGAAATTATAC 847
 Db |||||
 295 TCTTTCTTTATGCTAGAAATATTCAAATTACATTCAGTTATTTTGAATATATATAC 354
 QY 848 AATGAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCC 907
 Db |||||
 355 AACAGATTATTGTAAACTATAGTCACCCCTACTGATCTAGCAACAATGGTGTAC-TGCT 413
 QY 908 TCTATCTAACTGTATATTGTACCAGTTAACCAACCGTACTTTCATCCCCACTCCTCTCTA 967
 Db |||||
 414 TCTATCAAACTGTATATTGTAACTATTAAACCAACCTCTCTTCATCTCCTCTTCCCTTA 473
 QY 968 TCCTTCCCAACCTCTGATCACC-TCATTCTACTCTCTACCTCCATGAGATCCACTTTTTT 1026
 Db |||||
 474 CTTTTCCTAGTCTCTGGTTACCACCAATCTACTCTTTATCTTTATGAGATCCACATTTT 533
 QY 1027 AGTCCCACATGTGAGTAAGAAAATGCAATATTTGTCTTTTGTGCTGGCTTATTTCAC 1086
 Db |||||
 534 ATCTACTATATATAAGTGAGAAACATGTGATATTTGTCTTTCTGTACTTGGCTTATTTCAC 593
 QY 1087 TTAACATAATGACTTCTCTGTTCCATCCATGTTTGTGCAAAATGACAGGATTTCTGT 1141
 Db |||||
 594 TTAACATAATGACCTCCAATTCCCTCCATGTTTGTGTCATATTAAAGGATTTCTTT 648


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RESULT 4
BX382054      1201 bp      mRNA      linear      EST 08-MAY-2003
LOCUS      BX382054 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
DEFINITION      clone CS0DI073YL08 5-PRIME, mRNA sequence.
ACCESSION      BX382054
VERSION      BX382054.1 GI:30455012
KEYWORDS      EST.
SOURCE      Homo sapiens (human)
ORGANISM      Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1201)
Li, W.B., Gruber, C., Jessee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 559.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0DI073DF04QP1&cluster=559.f. Contact :
Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Faraday Avenue Genoscope sequence ID : CS0DI073DF04QP1.
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primer. Five prime end enriched, double-strand cDNA was
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ORIGIN
Query Match      20.7%;      Score 244;      DB 13;      Length 1201;
Best Local Similarity 67.8%;      Pred. No. 4.4e-40;
Matches 431;      Conservative 0;      Mismatches 170;      Indels 35;      Gaps 5;

QY      523 AGACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGGTGCATCTCAGCTTACTGC 582
Db      453 AGAAAGAGTCTTGTCTGTTGCTCAGGCTGGAGTGCATGATGGACCTCGGCTCACTGC 512
QY      583 AACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACCTCCCAAGTAGCTGGGACT 642
Db      513 AACCTCTGCCTCCCGATTCAAGCAATTCTCTGCCACAGCCTCTAAGTAGTAGGACT 572
QY      643 ACAGGCATGCACACAATGCCCAACTAATTTTGTATTTTGTAGTAGAGACGGGTTTTC 702
Db      573 ACACGCATGCACCAACACACCTGGCTAATTTTGTATTTTGTAGTAGGACGGGTTTCAC 632
QY      703 CATGTTGCCAGGCTGGCCTTGAACTCCTGGCCTCAACAATCCACTTGCCTCGGCCTCC 762
Db      633 CTGTTTGGCCAGGCTGGTCTCGAACTCCTGACCTCATGTGATCCGTCCACTTCAGCGTCC 692
QY      763 CAAAGTGTATGATTACAGGCGTGCAGCCACCGTGCCTGGCCTAAACATTATCTTTTCTT 822
Db      693 CAAAGTGTCTGGATTACAGGCATGAGCCACCGTGCCTGCCT----- 734
QY      823 TGTGTTGGGAACCTTTGAAATTATACAATGAATATTGTTAACTGTCACTCTCCCTGCTGTG 882
Db      735 --CTTTTAGTTATTTTAAATGTACAATAAATGTTGTTGACTGTAATCACCCCTGTTG 792
QY      883 CTATGGAACACTGGGACTTCTTCCCTCTATCTAACTGTATATTGTACAGTTAAACCAAC 942
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```

```

QY      943 CGTACTTCAATCCCACTCCTCTCTATCCTTCCCAACCTCTGATCACCTCATTTCTACTCTC 1002
Db      853 TT-----TCCCACTTCAACTACCTTCTTAAGCCTCTGGTAACGATCGTTCTGGTAT 905
QY      1003 TACCTCCATGAGATCCACT-----TTTTAGCTCCCACTGAGTAAGAAAATGCAATAT 1058
Db      906 CACCATGAGTTATTGTTTTCATTTTAGCTCCCAATAAGTGACACATGTGAATT 965
QY      1059 TTGTCCTTTCTGTGGCTGGCTTATTTCACCTTAACATAATGACTTCTGTTCCATCCATGTT 1118
Db      966 TTGTCCTTTCTGTGGCTGGCTTTTGTACCTTAAC--AATGACCTCCATTTCCATCC--CTT 1021
QY      1119 GCTGCAATGACAGGATTTCGTTCTTAAATTTCAAATT 1154
Db      1022 GTTGCAAGTGACAGCATCTCATTTTTTTTTTTTTT 1057

RESULT 5
AG128163      655 bp      DNA      linear      GSS 04-NOV-2001
LOCUS      Pan troglodytes DNA, clone: PTB-139D22.F, genomic survey sequence.
DEFINITION      Pan troglodytes DNA, clone: PTB-139D22.F, genomic survey sequence.
ACCESSION      AG128163
VERSION      AG128163.1 GI:16657328
KEYWORDS      GSS.
SOURCE      Pan troglodytes (chimpanzee)
ORGANISM      Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
BAC end sequences of Library PTB
Unpublished
2 (bases 1 to 655)
Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
Direct Submission
Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail:chimpbes@sc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
Tel:81-45-503-9111, Fax:81-45-503-9170)
Clones are derived from the chimpanzee BAC library PTB This BAC end
was generated during the R&D process and may have higher chance of
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/clone_lib="PTB Chimpanzee Male BAC Library"
ORIGIN
Query Match      20.5%;      Score 241.6;      DB 29;      Length 655;
Best Local Similarity 69.3%;      Pred. No. 1.5e-39;
Matches 413;      Conservative 0;      Mismatches 154;      Indels 29;      Gaps 5;

QY      573 AGCTTACTGCAACCTCTGCCTGCCAGTTCAAGCGATTCTCATGCTCCACCTCCCAAGT 632
Db      78 AGCTCACTGCAGTTCACCTCTCTGGGTTCAAGCAGTCTCTCCCGCTCAGCCTCCCAAGT 137
QY      633 AGCTGGGACTACAGGCATGCACCACAAATGCCCAACTAA-TTTTGTATTTTAGTAGAGA 691

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Db	138	AGCAGGGACACACAGGCACGTCGACCAACACACACTCAACTAAATTTTGTGATATTTTAGTAGAGA	197
QY	692	CGGGGTTTTGCCATGTTGCCAGGCTGGCCTTGAACCTCCTGGGCTCAAAACAATCCACTTG	751
Db	198	TGGGCTTTACCATGTTGCCAGGCTGGTTTCGAACCTCCTGAGCTCAGGCCATTTGCCCA	257
QY	752	CCTCGGC--CTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTGCCCTGGCCTAAACA	809
Db	258	TCTCAGCCTCTCCCGAAGTGCTGGGTTTACAGGTGTGAGCCATTTTGCCTGGCC-----	311
QY	810	TTTATCTTTTCTTTGTGGGAACTTTTGAATTTATACAAATGAATATTGTTAACTGTCA	869
Db	312	-----TCTTTTACTTATTTTAAACGTCACAGTAATTTATTGTTGACTTTTAG	359
QY	870	TCTCCCTGCTGTGCTATGGAACACCTGGGACTTCTTCCCTCTATCTAACTGTATATTGTA	929
Db	360	TCACCTGCTGTGCTATCAAATACTATATCTTATTTATCTGTCTAACTATATTTTGTGA	419
QY	930	CCAGTTAACCAACCGTACTTCATCCCCACTCCTCTCTATCCTTCCAAACCTCTGATCACC	989
Db	420	CCCATTAGCCATCCCCACTTCCTCTCCACAACGTGCTAGCCTTGCCAGTCTCTGGTAACCA	479
QY	990	TCATTCTACTCTCTACCTCCATGAGATCCA-----CTTTTTTAGCTCCCACATGTGAG	1042
Db	480	TCATTCTACTCCCTAGCTCCATAAGTTCAATTTGTTTTCATTTTAGCTCCCACAAATAAG	539
QY	1043	TAAGAAAATGCAATATTTGTTCTTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACTTC	1102
Db	540	TGAGAAATATGTGAAGTTTGTCTTTTCTGTGCCTGGCTTATTTCACTTAACATAATGACCTC	599
QY	1103	CTGTTCCATCCATGTTGCTGCAAAATGACAGGATTTCTGTTCTTAATTTCAATTAATA	1158
Db	600	CAG-TCCATCCATGTTGTTGCAAAAGACAGGACCTCATTTCTTTTATAGCTGAATA	654

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RESULT 6
AQ471624/c
LOCUS
DEFINITION
  AQ471624
  533 bp
  DNA
  linear
  GSS
  23-APR-1999
  CITBI-E1-2590G21.TR
  CITBI-E1 Homo sapiens genomic clone 2590G21,
  genomic survey sequence.
ACCESSION
  AQ471624
VERSION
  AQ471624.1
  GI:4655278
  GSS.
SOURCE
  Homo sapiens (human)
  ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  1 (bases 1 to 533)
  Zhao, S., Adams, M.D., Nierman, W., Malek, J., Shizuya, H., Simon, M. and
  Venter, J.C.
  Use of BAC End Sequences from Caltech Libraries for Sequence-Ready
  Map Building
  Unpublished (1997)
  Other_GSSs: CITBI-E1-2590G21.TF
  Contact: Shaying Zhao, William Nierman, Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: hbe@tigr.org
  Clones are available from Research Genetics (info@resgen.com). BAC
  end search page:
  http://www.tigr.org/tldb/humgen/bac_end_search/bac_end_search.html.
  Seq primer: M13 Reverse
  Class: BAC ends.
FEATURES
  Location/Qualifiers
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      /db_xref="taxon:9606"
      /clone="2590G21"
      /sex="male"

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/cell_type="sperm"
/clone_lib="CITBI-E1"
/note="Vector: pBeloBAC11; Site_1: EcoRI; Site_2: EcoRI;
CalTech Human BAC Library D"

ORIGIN
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Best Local Similarity 77.0%; Pred. No. 5.6e-39;
Matches 291; Conservative 0; Mismatches 87; Indels 0; Gaps 0;

QY 486 TATCCATCATCAAAACATTTATTTTATCTTTTAGACAGAGTCTCACTCTGTCAAC 545
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Db 462 TACCCATGCAAATTATCTTTTAATTTTATTTGTTGAGACAGAGTCTCACTTGTCACT 403
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 546 CAGGCTGGAGTGCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAG 605
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 402 CAGGCTGGAAACGAGTGGCACAACTCTGACTCACTGTCTACCTCTCGCGGGTTCAAG 343
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 606 CGATTCTCATGCCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCA 665
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 342 CAATTCTCTGCCTCAGCCTTTTGTAGTAGCTGGGATTACAGACATGCACCACCATGCCCA 283
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 666 ACTAATTTTGTATTTTGTAGTAGAGCGGGGTTTTGCCATGTTGCCAGGCTGGCCTTGA 725
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 282 GCTAATTTTGTATTTTGTAGTAGAGCAGAGTTTGTCCATGTTGGCCAGGCTGGTCTTGA 223
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 726 ACTCCTGGCCTCAAAACAATCCACTTGCCTCGGCCTCCCAAAGTGTTATGATTACAGGCGT 785
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 222 ACTCCTGGCCTCAAGTGATCCTCCTCGCTCGGCCTCCTAAAGTGTGGGATTACAGGCAT 163
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 786 GAGCCACCGTGCCTGGCCTAAACATTTATCTTTTCTTTGTGTGGGAACCTTTGAAATTAT 845
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||
Db 162 GAGCCACGTGCCCCGGCCTAATTATCCCTTTATCTTTAAAAATTAAAAATCAACAATGC 103
    ||||| ||||| ||||| ||||| ||||| ||||| ||||| ||||| |||||

QY 846 ACAATGAATTATTGTTAA 863
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Db 102 TTTTAAGTTTAGTATTAA 85
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RESULT 7	AG064829/c	LOCUS	AG064829	649 bp	DNA	linear	GSS 03-NOV-2001
DEFINITION			Pan troglodytes DNA, clone: PTB-054All.F, genomic survey sequence.				
ACCESSION			AG064829				
VERSION			AG064829.1	GI:16616631			
KEYWORDS			GSS.				
SOURCE			Pan troglodytes (chimpanzee)				
ORGANISM			Pan troglodytes				
			Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
			Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.				
REFERENCE			1				
AUTHORS			Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.				
TITLE			BAC end sequences of Library PTB				
JOURNAL			Unpublished				
REFERENCE			2	(bases 1 to 649)			
AUTHORS			Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T.D., Yada, T., Totoki, Y., Watanabe, H. and Sakaki, Y.				
TITLE			Direct Submission				
JOURNAL			Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical and Chemical Research (RIKEN), Genomic Sciences Center (GSC); 1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: chimpbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/, Tel: 81-45-503-9111, Fax: 81-45-503-9170)				
COMMENT			Clones are derived from the chimpanzee BAC library PTB This BAC end was generated during the R&D process and may have higher chance of clone tracking errors.				

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was generated during the R&D process and may have higher chance of
clone tracking errors.
PRIMERS
Sequencing: -21M13
LIBRARY
Vector      : pKS145
R.Site 1   : SacI
R.Site 2   : SacI

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Db 84 CATTTTTATTTTATTTTATTTTGACAGAGTCTCGCTCTGTGCGCCAGACTGGAGTGCAGT 143
QY 562 GGTGCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCTCCTCC 621
Db 144 GGTGGATCTTGGCTGACTGCAACCTCTGCCTTCTGGGTTCAAGCGATTCTCCTGCTCG 203
QY 622 ACCTCCAAAGTAGCTGGGACTACAGGCATGCACCACATGCCCCAACTAATTTTGTATTT 681
Db 204 GCCTCCGAGTAGCTGGGATTACAGACGCTGGCCACCATGCCGGCTAATTTTGTATTT 263
QY 682 TTAGTAGAGACGGGGTTTTTGCATGTTGCCAGGCTGGCCCTTGAACTCCTGGCCTCAAAC 741
Db 264 TTAGTAAACACGGGGTTTTTGCATGTTGGCCAGGCTGGTCTTGAACTCCTGGCCTCATTT 323
QY 742 AATCACTTGCCTCGGCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCTCGG 801
Db 324 GATCCACCTGCCTTGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACTGCACCCAG 383
QY 802 CCTAA 806
Db 384 CCTAA 388

RESULT 13
BX480642
LOCUS
DEFINITION
BX480642 633 bp mRNA linear EST 04-SEP-2003
DEFINITION DKFP686I24222_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
DEFINITION DKFP686I24222_5', mRNA sequence.

ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 633)
Bahr,A., Lauber,J., Mewes,H.W., Weil,B., Amid,C., Osanger,A.,
Fobo,G., Han,M. and Wiemann,S.
EST (Bahr,A., Lauber,J., Mewes,H.W., Weil,B., et al.)
Unpublished (2003)
Contact: MIPS

TITLE
JOURNAL
COMMENT
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing
consortium of the German Genome Project.
No sl sequence available.
This clone (DKFP686I24222) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin- Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..633
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFP686I24222"
/dev_stage="adult"
/lab_host="DH10B"
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cDNA-collection"

ORIGIN
Query Match 19.6%; Score 230.6; DB 13; Length 633;
Best Local Similarity 81.8%; Pred. No. 2.7e-37;
Matches 266; Conservative 0; Mismatches 59; Indels 0; Gaps 0;

QY 504 TTTATTTTATTTTATTTTATAGACAGAGTCTACTGTGTCACCCAGCGTGAGTGCAAGTGG 563
Db 37 TTTTATTTTATTTTATTTTATAGATGGAGTCTCGCTCTGTACCCAGCCGGAGTGCAAGTGG 96

QY 564 TGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCTCCTCAC 623
Db 97 TGCAATCTCAGCTCACTGCAACCTCTGCCTCCTGGTTCAACCGATTCTCCTGCTCAGC 156
QY 624 CTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTGTATTTT 683
Db 157 CTCCCAATAGCTGGGATTACTGTGCTGCCACCAACGCCAGCTAATTTTGTATTTT 216
QY 684 AGTAGACGGGGTTTTTGCATGTTGCCAGGCTGGCCCTTGAACTCCTGGCCTCAAACAA 743
Db 217 AGTAGAGATGGGGTTTCAACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAGGTGA 276
QY 744 TCCACTTGCCTCGGCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCTGGCC 803
Db 277 TCCGCTGCTCGGCTCCCAAAGTGTGGGATTACAGCATGAGCCACCATGCTGCTGACC 336
QY 804 TAAACATTTATCTTTTCTTTTGTGTT 828
Db 337 CTGTTTCTTTTCTTTTCTTTTCTT 361

RESULT 14
AW963663/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
AUTHORS
1 (bases 1 to 727)
Hegde,P., Qi,R., Abernathy,K., Dharap,S., Gaspard,R., Gay,C.,
Holt,I.E., Saeed,A.I., Sharov,V., Lee,N.H., Yeatman,T.J. and
Quackenbush,J.

TITLE
JOURNAL
COMMENT
Assessment of gene expression patterns in a model of colon tumor
metastasis using a 19,200 element cDNA microarray
Unpublished (2000)
Contact: John Quackenbush
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 3528
Fax: 301 838 0208
Email: johnq@tigr.org
Plate: 190
Seq primer: Reverse.
Location/Qualifiers
1..727
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGH"
/note="Vector: pBluescriptSKm"

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/db_xref="taxon:9606"
/clone_lib="MAGE resequences, MAGH"
/note="Vector: pBluescriptSKm"

ORIGIN
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Best Local Similarity 78.8%; Pred. No. 2.7e-37;
Matches 275; Conservative 0; Mismatches 74; Indels 0; Gaps 0;

QY 497 TCAAAACATTTATTTTATTTTATTTTAGACAGAGTCTCACTCTGTACCCAGGCTGGAGT 556
Db 563 TAAAAAAATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTTATTTT 504
QY 557 GCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATG 616
Db 503 GCAATGGCATGATCTTGATTCACTGCAACCTCCGCTCCAGGTTCAAGTGATTCTCCTG 444
QY 617 CCTCCACCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTG 676
Db 443 CCTCAGCCTCCCAAGTAGCTGGGACTACAGGCGTGACACCATGCCCGGCTAATTTTG 384

Db 278 CCTCAGCCTCCCAAGTAGCTGGATTACAGGCACCCGCCACCATGCCTGGCTAATTTTG 337
QY 677 TATTTTATGAGACGGGGTTTGGCCATGTTGCCAGGCTGCGCTTGAACCTCCTGGCT 736
Db 338 TGTTTTATGAGACAGGATTTCACCATGTTGGCCAGGCTGTTCTCGAATCCTGACCT 397
QY 737 CAAACAATCCACTTGCTCGGCTCCCAAAAGTGTATGATTACAGGCGTGAGCCACCGTG 796
Db 398 CGGGTGATCCACCGCCTTGGTCTCCCAAAGTGACGGGCTTACAGGCGTGAGCCACCGTG 457
QY 797 CCTGGCCTAAACATTTATCTTTTCTTTGTTGTTGGGAACCTTTGAAATTATACAATGAATTA 856
Db 458 CCCGGCCTA--TCTACTCTATTACTTTGAATTCCTGGCCACGCTTGTCCCTGCCACA 514
QY 857 TTGTTAATGTTCATCTCCCTGCTGCTATGGAACACTGGGACTTCTTCCCTCTATCTAA 916
Db 515 GTGCCCTTGCTTATCTGGCTCCTTCCATAGGGATCCAGAGACATCTTCTCTCTCT 574
QY 917 CTGTATATTGTACCAGTTAACCAACCGTACTTCAATCCCACTCCTCTCTATCCTTCCCA 976
Db 575 CTCTCTCTTGTCTTATCTGGCTCCTTGCATANGGATCCAGAGACATCTCTCTCTCT 634
QY 977 ACCTCTGATCACCTCATCTCTCTCTCTACCTCCATGAGATCCACTTTTTTAGTCTCCACA 1036
Db 635 CTCTCTCTCTCTCAATNTNTCTCTCTTTTGTGAACAGAGCCCTGCTCTGGGGCTCCACA 694
QY 1037 TGTGAGT 1043
Db 695 CTGGAAT 701

RESULT 17
AQ346434/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
FEATURES
source

AQ346434 705 bp DNA linear GSS 07-MAY-1999
RPCI11-101K7.TJB RPCI-11 Homo sapiens genomic clone RPCI-11-101K7,
genomic survey sequence.
AQ346434
AQ346434.1 GI:4171330
GSS.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 705)
Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
Venter,J.C.
Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
Map Building
Unpublished (1997)
Other GSSs: RPCI11-101K7-TV
Contact: Shaying Zhao, William Nierman, Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850
Tel: 301 838 0200
Fax: 301 838 0208
Email: hbe@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from
Research Genetics (info@resgen.com). BAC end search page:
http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Seq primer: SP6
Class: BAC ends.
Location/Qualifiers
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/db_xref="GDB:7538646"
/db_xref="taxon:9606"
/clone="RPCI-11-101K7"

/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
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Query Match 19.6%; Score 230.2; DB 28; Length 705;
Best Local Similarity 84.4%; Pred. No. 3.2e-37;
Matches 259; Conservative 0; Mismatches 48; Indels 0; Gaps 0;
QY 508 TTTTATTTTATTTTATGACAGAGTCTCACTCTGTCAACCCAGGCTGAGTGGTGCC 567
Db 327 TTTTATTTTATTTTATGAGTGGAGTCTCACTCTATTGCCAGGCTGAAGTGCAGTGGTGCC 268
QY 568 ATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACCTCC 627
Db 267 ATCTCGGCTCACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCCTGCCCTCAGCCTCC 208
QY 628 CAAGTAGCTGGGACTACAGGCATGCAACCAATGATGCCCAACTAATTTTGTATTTTAGTA 687
Db 207 CAAGTAGCTGGGATTACAGGCGTGTGCCACCATGCCACGCTAATTTTGTATTTTAGTA 148
QY 688 GAGACGGGTTTGGCCATGTTGCCAGGCTGGCCTTGAACCTCTGGCCTCAACAATCCA 747
Db 147 GACACGGGTTTGGCCATGTTGGCCAGGCTGGTCTTGACCTCCTAACCTCAGGTGATTCT 88
QY 748 CTTGCCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCCTAAA 807
Db 87 CCTGCCCTCAGCCTCCCAAGTGTCTGGGATTACAGGTGTGAGCCACTGCACCTGGCCTGGA 28
QY 808 CATTAT 814
Db 27 TTTGAAT 21

RESULT 18
BC035078/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
MEDLINE
PUBMED
REFERENCE

BC035078 2768 bp mRNA linear HTC 19-NOV-2003
Homo sapiens skeletrophin, mRNA (cDNA clone IMAGE:5260457), with
apparent retained intron.
BC035078
BC035078.1 GI:23272436
HTC.
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2768)
Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
Villalón,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
Fahey,J., Helton,E., Kettman,M., Madan,A., Rodriguez,S.,
Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smalusz,D.E.,
Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
Generation and initial analysis of more than 15,000 full-length
human and mouse cDNA sequences
Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
22388257
12477932
2 (bases 1 to 2768)

AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgabbs-re@mail.nih.gov
Tissue Procurement: Miklos Palkovits, M.D., Ph.D.
cDNA Library Preparation: Michael J. Brownstein (NHGRI) & Shiraki Toshiyuki and Piero Carninci (RIKEN)
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Institute for Systems Biology
<http://www.systemsbio.org>
contact: amadan@systemsbiology.org
Anup Madan, Jessica Fahey, Erin Helton, Mark Kettelman, Anuradha Madan, Stephanie Rodrigues, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAX Plate: 73 Row: c Column: 6
This clone has the following problem: retained intron.

FEATURES Location/Qualifiers
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/db_xref="taxon:9606"
/clone="IMAGE:5260457"
/tissue_type="Brain, hippocampus"
/clone_lib="NIH_MGC_95"
/lab_host="DH10B"
/note="Vector: pBluescript"

ORIGIN
Query Match 19.6%; Score 230.2; DB 11; Length 2768;
Best Local Similarity 81.0%; Pred. No. 2.8e-37;
Matches 268; Conservative 0; Mismatches 63; Indels 0; Gaps 0;
QY 504 TTTATTTTATCTTTTGTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGG 563
Db 2739 TTTGTTTTTTTGTCTTTGAGACGGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGG 2680
QY 564 TGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCAC 623
Db 2679 CCAGATCTTGGCTCACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCCACCTCAGC 2620
QY 624 CTCCCAAGTAGCTGGGACTACAGGCTACAGGCTACAGGCTTGAACCTTGAACCTTGAATTTT 683
Db 2619 CTCCCAAGTAGCTGGGACTACAGGCTACAGGCTTGAACCTTGAACCTTGAATTTT 2560
QY 684 AGTAGAGACGGGTTTGGCCATGTTGCCAGGCTGGCCTTGAACCTTGAACCTTGAATTTT 743
Db 2559 AGTAGAGATGGGTTTGGCCATGTTGGCAAGGCTGGTCTCCAACTCTGGCCACAGGTGA 2500
QY 744 TCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCCTGGCC 803
Db 2499 TCCTCCCACTTGGCTCACAAGTGTGGGATTACAGGCGTGAGCCACTGTGCCTGGCT 2440
QY 804 TAAACATTTATCTTTCTTTGTTGGGAAC 834
Db 2439 GGTTTTTTTCTTTTTTTTTTTTGTGAGAC 2409

RESULT 19
LOCUS AQ046370/c
DEFINITION RPC111-34B11.TJ RPCI-11 Homo sapiens genomic clone RPCI-11-34B11, genomic survey sequence.
ACCESSION AQ046370
VERSION AQ046370.1 GI:3315297
KEYWORDS GSS.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 393)
AUTHORS Adams,M.D., Rounsley,S.D., Zhao,S., Field,C.E., Bass,S., Linher,K., Golden,K., Berry,K., Granger,D., Suh,E., Wible,C., de Jong,P. and Venter,J.C.
TITLE Use of BAC End Sequences for Sequence-Ready Map Building (1998)
JOURNAL Unpublished (1998)
COMMENT Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering>) or from Research Genetics (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/humgen/bac_end_search/bac_end_search.html
Class: BAC ends.

FEATURES Location/Qualifiers
source 1..393
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7512706"
/db_xref="taxon:9606"
/clone="RPCI-11-34B11"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"
/note="Vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI; RPC111 Human Male BAC Library"

ORIGIN
Query Match 19.5%; Score 229.8; DB 28; Length 393;
Best Local Similarity 85.9%; Pred. No. 4.2e-37;
Matches 255; Conservative 0; Mismatches 42; Indels 0; Gaps 0;
QY 508 TTTTATTCTTTTGTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGTGCC 567
Db 304 TTTTATTCTTTTGTAGATGGAGTCTCACTCTATTGCCAGGCTGAAGTGCAGTGGTGCC 245
QY 568 ATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACCTCC 627
Db 244 ATCTCGGCTCACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCCTGCCTCAGCCTCC 185
QY 628 CAAGTAGCTGGGACTACAGGCTACAGGCTACAGGCTTCAAGCGATTCTTGTATTTTAGTA 687
Db 184 CAAGTAGCTGGGATTACAGGCTGTGCCACCATGCCAGCTAATTTTGTATTTTAGTA 125
QY 688 GAGACGGGGTTTGGCCATGTTGCCAGGCTGGCCTTGAACCTCCTGGCCTCAAAACAATCCA 747
Db 124 GACACGGGGTTTGGCCATGTTGCCAGGCTGGTCTTGACCTCCTAACCTCAGGTGATTCT 65
QY 748 CTTGCCCTCGGCTCCCAAGTGTATTATACAGGCGTGAGCCACCGTGCCTGGCCT 804
Db 64 CTTGCCCTCAGCCTCCCAAGTGTCTGGGATTACAGGTGTGAGCCACTGCACCTGGCCT 8

RESULT 20
LOCUS BZ611126/c
DEFINITION WHADL87TF Human MCF7 breast cancer cell line library (MCF7_1) Homo sapiens genomic clone MCF7_1-21P6, genomic survey sequence.
ACCESSION BZ611126
VERSION BZ611126.1 GI:31519687
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

JOURNAL Unpublished (1998)
COMMENT Other_GSSs: CIT-HSP-2311P23.TR
Contact: Mark Adams
Department of Eukaryotic Genomics
The Institute for Genomic Research
9712 Medical Center Dr., Rockville, MD 20850, USA
Tel: 301 838 0200
Fax: 301 838 0208
Email: mdadams@tigr.org
Clones are available from Research Genetics (info@resgen.com). BAC
end search page:
http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.
Seq primer: M13-21
Class: BAC ends.

FEATURES
source Location/Qualifiers
1..452
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="2311P23"
/sex="Male"
/cell_type="Sperm"
/clone_lib="CIT-HSP"
/note="Vector: pBelobAC11; Site_1: HindIII; Site_2:
HindIII"

ORIGIN
Query Match 19.5%; Score 229; DB 28; Length 452;
Best Local Similarity 82.6%; Pred. No. 6e-37;
Matches 262; Conservative 0; Mismatches 55; Indels 0; Gaps 0;
QY 508 TTTTATCTTTTATGACAGAGTCTGTCACCCAGGCTGGAGTGCAGTGGTCC 567
Db 432 TTTTATCTTTTATGACAGGAGTCTGTCACACAGGCTGGAGTGCAGTGGTCA 373
QY 568 ATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACCTCC 627
Db 372 ATCTCAGCTCACTGCAGCCTCCACGCCAGATTCAAGCGATTCTCCTGCCCTCAGCCTCC 313
QY 628 CAAGTAGCTGGGACTACAGGCATGACCAATGCCCAATGCTGAACTCTGAGCTCAAAATCCA 687
Db 312 CAAGTAGCTGGAATTACAGATGTGCACCAACCAAGCTGCTGAACTCTGAGCTCAAAATCCA 253
QY 688 GAGACGGGTTTGGCCATGTTGCCAGGCTGGCTTGAATCTGAGCTGAGCTCAAAATCCA 747
Db 252 GAGATGGGTTTGGCCATGTTGGCCAGGCTGCTCAAACTCTGAGCTCAAAATCCA 193
QY 748 CTTGCCCTCGGCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCTCAAA 807
Db 192 CCTGCCCTTGGCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCGTGCCTGGCTCAAA 133
QY 808 CATTATCTTTCTTTG 824
Db 132 CAGGTATTTTATAG 116

RESULT 23
AG167597 678 bp DNA linear GSS 09-JAN-2002
LOCUS Pan troglodytes DNA, clone: RP43-035L11.T7, genomic survey
DEFINITION sequence.
ACCESSION AG167597
VERSION AG167597.1 GI:16697275
KEYWORDS GSS.
SOURCE Pan troglodytes (chimpanzee)
ORGANISM Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
1
REFERENCE
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE BAC end sequences of Library RPCI-43
JOURNAL Unpublished

REFERENCE 2 (bases 1 to 678)
AUTHORS Fujiyama, A., Hattori, M., Toyoda, A., Taylor, T. D., Yada, T.,
Totoki, Y., Watanabe, H. and Sakaki, Y.
TITLE Direct Submission
JOURNAL Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
1-7-22 Suehiro-chou, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
(E-mail: chimpanbes@gsc.riken.go.jp, URL: http://hgp.gsc.riken.go.jp/,
Tel: 81-45-503-9111, Fax: 81-45-503-9170)
COMMENT Clones are derived from the chimpanzee BAC library RPCI-43. This BAC
end was generated during the R&D process and may have higher chance
of clone tracking errors.
PRIMERS
Sequencing: T7
LIBRARY Vector : pBACe3.6
R.Site 1 : EcoRI
R.Site 2 : EcoRI.
Location/Qualifiers
1..678
/organism="Pan troglodytes"
/mol_type="genomic DNA"
/db_xref="taxon:9598"
/clone="RP43-035L11.T7"
/sex="male"
/cell_type="lymphocytes"
/clone_lib="RPCI-43 Chimpanzee Male BAC Library"

FEATURES
source
Query Match 19.5%; Score 229; DB 29; Length 678;
Best Local Similarity 73.7%; Pred. No. 5.8e-37;
Matches 289; Conservative 0; Mismatches 103; Indels 0; Gaps 0;
QY 504 TTTATTTTATCTTTTATGACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGG 563
Db 255 TTTTATTTTATCTTTTATGAGATAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGG 314
QY 564 TGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCCCTCCAC 623
Db 315 CATGATCTGGCTTACTGCAACTCTCGCCTCTGGTTCAAGCAGTTCTCCTGTTTCAGC 374
QY 624 CTCCCAAGTAGCTGGGACTACAGCATGCACCACCAATGCCCAACTAATTTTGTATTTT 683
Db 375 CTCCCAAGTAGCTGGGATTACAGGCATACACCACCAATGCCCAGCTAATTTTGTATTTT 434
QY 684 AGTAGACGGGGTTTGGCCATGTTGCCAGGCTGGCCCTGAACTCTGGCCCTCAACAA 743
Db 435 AGTAGACAGGGTTTGGCCATGTTGCCAGGAGGTTCTTGAACCCATGACCTCAGGTGA 494
QY 744 TCCACTTGCCTCGGCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGCC 803
Db 495 TCCGCCACTTTGGCCTCCCAAGAGTGTAGGATTTTCAGGCGTGAGCCACACCTGGCC 554
QY 804 TAAACATTTATCTTTTCTTTGTGTGGAACTTTGAAATATACAAATGATTTGTTAA 863
Db 555 TTTTCTCTATCTNTNNTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCTTTTCT 614
QY 864 CTGTCACTCCCTGCTGTGCTATGGAACACTG 895
Db 615 TGTTCCCAAGCTAATATGCAAGGGGCGATG 646

RESULT 24
BH152879/c 504 bp DNA linear GSS 27-AUG-2001
LOCUS UP 297-17A.T7 RPCI11 Human Male BAC Library Homo sapiens genomic
DEFINITION clone 297-17A, genomic survey sequence.
ACCESSION BH152879
VERSION BH152879.1 GI:15317004
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

REFERENCE 1 (bases 1 to 504)
AUTHORS Cheung,V.G., Dalrymple,H.I., Narasimhan,S., Watts,J., Schuler,G., Raap,A.K., Morley,M. and Bruzel,A.
TITLE A resource of mapped human bacterial artificial chromosome clones
JOURNAL Genome Res. 9 (10), 989-993 (1999)
MEDLINE 99455100
PUBMED 10523527
COMMENT Contact: Arcaro MA, Morley M, Burdick J, Cheung VG
Department of Pediatrics
University of Pennsylvania
3516 Civic Center Blvd, ARC 516, Philadelphia, PA 19104, USA
Tel: 215 590 2664
Fax: 215 590 3709
Email: mlennox@mail.med.upenn.edu
Plate: 297 row: A column: 17
Seq primer: T7
Class: BAC ends.

FEATURES
source
1..504
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="297-17A"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPC111 Human Male BAC Library"
/note="Vector: pBACe3.6; RPC111 Human Male BAC Library"

ORIGIN
Query Match 19.4%; Score 228.6; DB 28; Length 504;
Best Local Similarity 82.9%; Pred. No. 7.2e-37;
Matches 261; Conservative 0; Mismatches 54; Indels 0; Gaps 0;

QY 503 ATTTATTTTATCTCTTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGAGTGCAGTG 562
|||||
Db 501 ATTTATATTATTTTITAGATGGAGTCTCGCTCTGTCACCCAGGCTGAGTGCAGTG 442
|||||
QY 563 GTGCCATCTCAGCTTACTGCAACCTCTGCGCTGCCAGGTTCAAGCGATTCTCATGCCCTCCA 622
Db 441 GCACAATCTCAGTCTACTGCAACCTCCGCCCTCCGGCTTCAAGCGATTCTCTGCCTCAG 382
|||||
QY 623 CTCCCAAAGTAGCTGGGACTACAGGCATGCACACAATGCCCAACTAATTTTGTATTTT 682
Db 381 CTCTCCAAAGTAGCTGGGACTACAGGCATGTGCCACCATGCTGGCTAATTTTGTATTTT 322
|||||
QY 683 TAGTAGAGACGGGTTTGTGCCATGTTGCCAGGCTGGCCTTGAACCTCCGGCCTCAACA 742
Db 321 TAACAGAGATGGGTTTTCGCCATGTTGGCCAGGTGATCTCAAACTCCTGACCTCAGGTG 262
|||||
QY 743 ATCCACTTGCCTCGGCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGC 802
Db 261 ATCCGCTGCCTCGGCTCCCAAAGTGTCTGGATTACAGGCATGAGCCACCGTGCCTAGC 202
|||||
QY 803 CTAAACATTTATCTT 817
Db 201 CTACTTTTATTTT 187
|||||

RESULT 25
AQ788367
LOCUS
DEFINITION HS_3135_A2_E11_MR CIT Approved Human Genomic Sperm Library D Homo sapiens genomic clone Plate=3135 Col=22 Row=I, genomic survey sequence.
ACCESSION AQ788367
VERSION AQ788367.1 GI:5695991
KEYWORDS GSS.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 751)

AUTHORS Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.
TITLE Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
MEDLINE 99380589
PUBMED 10449764
COMMENT Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones may be purchased from Research Genetics (info@resgen.com).
BAC end Web Server: http://www.htsc.washington.edu
Plate: 3135 row: I column: 22
Seq primer: M13 Reverse
Class: BAC ends
High quality sequence stop: 751.
Location/Qualifiers
1..751
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"
/clone="Plate=3135 Col=22 Row=I"
/sex="male"
/clone_lib="CIT Approved Human Genomic Sperm Library D"
/note="Organ: sperm; Vector: pBelobAC11; BAC Clones in E-Coli DH10B"

ORIGIN
Query Match 19.4%; Score 228.4; DB 28; Length 751;
Best Local Similarity 75.2%; Pred. No. 7.6e-37;
Matches 297; Conservative 0; Mismatches 97; Indels 1; Gaps 1;

QY 502 CATTTATTTTATCTTTTGTAGACAGAGTCTCACTCTGTCACCCAGGCTGAGTGCAGT 561
|||||
Db 188 CTTTCTTTTITTTTITTTTGTAGACAGAGTCTCACTCTGTGCTGCCAGGCTAGATACAGT 247
|||||
QY 562 GGTGCCATCTCAGCTTACTGCAACCTCTGCTGCTGCCAGGTTCAAGCGATTCTCATGCTCC 621
Db 248 GGTGCGATCTCGGCTCACTGCAACCTCTGCTTCCAGGTCGAAGCGATTCTCCTGCCTCA 307
|||||
QY 622 ACTCCCAAGTAGCTGGGACTACAGGCATGCACCAATGCCCAACTAATTTTGTATTT 681
Db 308 GCCTCCCGAGTAGCTGGGACTATAGGCACGTGCCACACACACTGGCTAATTTCTGTATTT 367
|||||
QY 682 TTAGTAGAGACGGGTTTGTCCCATGTTGCCAGGCTGGCCTTGAACCTCCTGGCCTCAAAC 741
Db 368 TTAGTAGAGACAGGGTTTACCATGTTGGCCAGGCTGCTCGAACTCCTGACTCAGGT 427
|||||
QY 742 AATCCACTTGCTCGGCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGG 801
Db 428 GATCCACCTGTCTTGGCCTCCCAAAGTGTGGGATTACAGGCATGAGCCACCGTGCCTGG 487
|||||
QY 802 -CCTAAACATTTATCTTTTCTTTTGTGTTGGGAACCTTGAATATATACAATGAATTATGT 860
Db 488 CCTGCACTCCTATTTCTTCAATGGAATGTACCTTCTTCTTGCCTTCTGATTGCTTNC 547
|||||
QY 861 TAACTGTCACTCTCCCTGTGTGCTATGGAACACTG 895
Db 548 TTCTTGCCCTTTTCTTCTCTCTGCAATCCAAATACTG 582
|||||

RESULT 26
BE075068/c
LOCUS
DEFINITION BE075068-310100-002-g11 BT0585 Homo sapiens linear mRNA EST 09-JUN-2000
ACCESSION BE075068
VERSION BE075068.1 GI:8423577
KEYWORDS EST.

QY 805 AAACATTATCTTTTCTTTG 824
Db 381 CTGTCATCNTTTTGTGTTG 400

RESULT 28
A1114733
LOCUS
DEFINITION
HA1332 Human fetal liver cdna library Homo sapiens cDNA, mRNA
sequence.
ACCESSION
A1114733
VERSION
A1114733.1 GI:6360078
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 583)
AUTHORS
Yu,Y., Zhang,C., Luo,L., Ouyang,S., Li,W., Wu,J., Zhou,S., Liu,M.
and He,F.
TITLE
Expression profile analysis of a human fetal liver cdna library
JOURNAL
Unpublished (1998)
COMMENT
Contact: Yongtao Yu
Department of Hematology
Beijing Institute of Radiation Medicine
27 Taiping Road, Beijing 100850, P.R.China
Tel: 0086-10-68159479
Fax: 0086-10-68214653
Email: Yyt48@yahoo.com.

FEATURES
source
1..583
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="liver"
/dev_stage="fetal"
/lab_host="MC1061/P3"
/clone_lib="Human fetal liver cdna library"
/note="Vector: pCDNA1"

ORIGIN
Query Match 19.3%; Score 227.4; DB 9; Length 583;
Best Local Similarity 78.0%; Pred. No. 1.3e-36;
Matches 273; Conservative 0; Mismatches 77; Indels 0; Gaps 0;

QY 497 TCAAAACATTTATTTTATCTTTTGTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGT 556
Db 226 TCAAAACATTTTATTTTGTAGATGGAGTCTCCCTCTGTCAACCAGGCTGGAGT 285

QY 557 GCAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATG 616
Db 286 GCAGTGGTGCACTCTCGACTCATTGCACCCCTCATCTTTGGGGTTCAAGTGATTCTCCTG 345

QY 617 CCTCCACCTCCCAAGTAGCTGGGACTACAGGATGCACCAATGCCCAACTAATTTTGT 676
Db 346 CCTCAGGCTCTCAAGTAGCTGGGATTACAGGCATGCACCAAGGCCAGCTAATTTTGT 405

QY 677 TATTTTGTAGAGACGGGGTTTTCATGTTGGCCAGGCTGGCCTTGAACTCCTGGCCT 736
Db 406 TATTTTGTAGAGACGGGGTTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCT 465

QY 737 CAAACAATCCACTTGCTCGGCCTCCCAAAGTGTTATGATTACAGGCGTGAGCCACCGTG 796
Db 466 CAGGTGATCCACCCACCTTGGCCTCTTGAAGTGTGGGATTATAGACGTGAGCCACTGTG 525

QY 797 CTGGCCTAAACATTTATCTTTTCTTTGTGTGGGAACCTTTGAAATTATA 846
Db 526 CTGGCCTAAAGATTATTATTATANAAAAATTATCCAATTATGAAGGATA 575

RESULT 29
AL712182

LOCUS
DEFINITION
DKFZp686E1487_r1 686 (synonym: hlcc3) Homo sapiens cDNA clone
AL712182
ACCESSION
AL712182
VERSION
AL712182.1 GI:19695537
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
1 (bases 1 to 592)
AUTHORS
Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and Wiemann,S.).
TITLE
EST (Poustka,A., Wellenreuther,R., Mewes,H.W., Weil,B. and
Wiemann,S.)
JOURNAL
Unpublished (1999)
COMMENT
Contact: MIPS
MIPS
Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany
This is the 5' sequence of the clone insert
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;
sequenced by DKFZ (German Cancer Research Center,
Heidelberg/Germany) within the cDNA sequencing consortium of the
German Genome Project.
No sl sequence available.
This clone (DKFZp686E1487) is available at the RZPD in Berlin.
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES
source
1..592
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="DKFZp686E1487"
/dev_stage="adult"
/lab_host="DH10B"
/clone_lib="686 (synonym: hlcc3)"
/note="Vector: pTriplEx2; Site_1: SfiIA; Site_2: SfiIB;
cDNA-collection"

ORIGIN

Query Match 19.3%; Score 227.4; DB 9; Length 592;
Best Local Similarity 79.2%; Pred. No. 1.3e-36;
Matches 270; Conservative 0; Mismatches 71; Indels 0; Gaps 0;

QY 504 TTATATTTTATTTTATTTTATAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGG 563
Db 252 TCTACTTTTATTTTGTAGACAGAGTCTCACTCTGTCACTCAGGCTAGAGTGCAATGG 311

QY 564 TGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCAC 623
Db 312 TGAATCTCAGCTCACTGCAACTTCGGCTCCAGGTTCAAGCGATTCTCTCGCTCAGC 371

QY 624 CTCCCAAGTAGCTGGGACTACAGGCATGCACCAATGCCCAACTAATTTTGTATTTT 683
Db 372 CTCCCAAGTAGCTAGAACTACAGGCGCCGCCACCGCTGGCTAATTTTGTATTTT 431

QY 684 AGTAGAGACGGGGTTTTCCTATGTTGCCAGGCTGGCCTTGAACCTCCTGGCCTCAAAACAA 743
Db 432 AGTAGAGAAAGGGTTTTCACCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGA 491

QY 744 TCCACTTGCTCGGCCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCC 803
Db 492 TCCAAACGCGCTCGGCCTCCCAAAGTACTGAGATTACAGGCGTGAGGCACGTGCGCCGCC 551

QY 804 TAAACATTTATCTTTTCTTTGTGTGGGAACCTTTGAAATTA 844
Db 552 CAGTTTTTCTACTTCTATATGAGATGAATATATATTCATTTTA 592

RESULT 30
BC015230/c
LOCUS
BC015230 1638 bp mRNA linear HTC 12-SEP-2002

Homo sapiens, clone IMAGE:3899552, mRNA.
BC015230
ACCESSION BC015230.1 GI:21955365
VERSION
KEYWORDS HTC.
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1638)
Strausberg,R.
Direct Submission
Submitted (01-OCT-2001) National Institutes of Health, Mammalian
Gene Collection (MGC), Cancer Genomics Office, National Cancer
Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
USA
NIH-MGC Project URL: <http://mgc.nci.nih.gov>
Contact: MGC help desk
Email: cgapps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Sequencing Group at the Stanford Human Genome
Center, Stanford University School of Medicine, Stanford, CA 94305
Web site: <http://www-shgc.stanford.edu>
Contact: (Dickson, Mark) mcd@paxil.stanford.edu
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,
R. M.

Clone distribution: MGC clone distribution information can be found
through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
Series: IRAK Plate: 14 Row: 1 Column: 12
This clone has the following problem: frame shifted.
Location/Qualifiers
1. 1638
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3899552"
/tissue type="Pancreas, epithelioid carcinoma"
/clone_lib="NIH_MGC_70"
/lab host="DH10B"
/note="Vector: pCMV-SPORT6"

FEATURES
source

ORIGIN

```

RESULT 31
AV756491/c
LOCUS       AV756491          551 bp      mRNA      linear      EST 19-OCT-2000
DEFINITION  AV756491 BM Homo sapiens cDNA clone BMFA5E04 5', mRNA sequence.
ACCESSION   AV756491
VERSION     AV756491.1  GI:10914339
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 551)
AUTHORS     Gu,J., Zhao,M., Huang,Q., Xu,X., Li,Y., Peng,Y., Song,H., Xiao,H.,
            Gu,Y., Li,N., Qian,B., Liu,F., Qu,J., Gao,X., Cheng,Z., Xu,Z.,
            Zeng,L., Xu,S., Gu,W., Tu,Y., Jia,J., Fu,G., Ren,S., Zhong,M.,
            Lu,G., Yang,Y., Gao,G., Wang,Z., Zhang,Q., Chen,S., Han,Z. and
            Chen,Z.
TITLE       Homo sapiens cDNA BM clones
JOURNAL     Unpublished (2000)
COMMENT     Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919 (ex.45)
            Fax: 86-21-50801922
            Email: hanzg@chgc.sh.cn
            This clone is available at CHGC in Shanghai.

FEATURES             Location/Qualifiers
     source           1..551
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="BMFA5E04"
                     /tissue_type="Bone marrow"
                     /cell_type="CD34+ hematopoietic stem/progenitor cell"
                     /lab_host="BM25.8"
                     /clone_lib="BM"
                     /note="Vector: pTriplex2; Site_1: sfiIA; Site_2: sfiIB"

ORIGIN
Query Match      19.3%;   Score 227.2;   DB 9;   Length 551;
Best Local Similarity 84.2%;   Pred. No. 1.4e-36;
Matches 256;   Conservative 0;   Mismatches 48;   Indels 0;   Gaps 0;

QY  504  TTTATTTTATTCTCTTTTAGACAGAGTCTCACTCTGTCAACCCAGGCTGGAGTGCAGTGG 563
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   391  TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT TTTT
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  564  TGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCTCCAC 623
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   331  CGCAATCTCAGCTCACTGCAACCTCCGCCTCCAGGTTCAAGCGATTCTCTGCTCAGC 272
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  624  CTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTGTATTTT 683
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   271  CTCCCTAGTAGCTGGGACTACAGGCATGGCCACTACCCAGCTAATTTTGTATGTT 212
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  684  AGTAGAGACGGGTTTTTGCCATGTTGCCAGGCTGGCCTTGAACCTCCTGGCCTCAACAA 743
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   211  AGTAGAGAGGAGTTTCACCATGTTGGCCAGGCTGGTCTTGAACTCCTGACCTCAAGTGA 152
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  744  TCCACTTGCTCGGCCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCC 803
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db   151  TCTGCCCTCTTCAGCCTCCCAAAGTCTGGGATTACAGGCATGAGCCACCCAGCCAGCC 92
      ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY  804  TAAA 807
      ||| |||
Db   91  TAGA 88

RESULT 32
AI114557
LOCUS       AI114557          679 bp      mRNA      linear      EST 11-NOV-1999
DEFINITION  HAI140 Human fetal liver cDNA library Homo sapiens cdNA, mRNA

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Db 330 TGGGGTGAATGGTGTGATCTCGGCCCACTGCAACCTCTGCCTCCTGGGTTCAAGCAATT 271
QY 611 CTATAGCCTCACCTCCCAAGTAGCTGGGACTACAGGCATGACCAACAATGCCCAACTAA 670
Db 270 CTTGTGCCTCAGCCTCCCGAGTAGCTGGGACTACAGGCATGTGCCACCAACCCAGCTAA 211
QY 671 TTTTGTATTTTAGTAGAGACGGGGTTTTGCCATGTTGCCAGGCTGGCCTTGAACTCC 730
Db 210 TTTTGTATTTTAGTAGAGACGGGGTTTCACCATGTTGCCCTAGGCTGGTCTCAAACTCC 151
QY 731 TGGCCTCAAAACAATCCACTTGCCCTCGGCCTCCCAAAGTGTATGATTACAGGCGTGAGCC 790
Db 150 TGACCTCAGGTGATCCACCTGCCTTGCTTCCCAAAGTTCCTGGGATTACAGGCAAGGCC 91
QY 791 ACCGTGCCTGGCCTAAACATTTATCTTTCT 821
Db 90 ACCATGCCCGGCTGAACAGATTTTTTTTTT 60

RESULT 38
AI732789/c
LOCUS
DEFINITION
AI732789 484 bp mRNA linear EST 14-JUN-1999
ab09h12.x5 Stratagene lung (#937210) Homo sapiens cDNA clone
IMAGE:840359 3' similar to contains Alu repetitive element; mRNA
sequence.
ACCESSION
AI732789
VERSION
AI732789.1 GI:5053902
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 484)
AUTHORS
NCI/NIDR-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
TITLE
National Cancer Institute / National Institute of Dental Research,
Cancer Genome Anatomy Project (CGAP), Tumor Gene Index
JOURNAL
Unpublished (1997)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
This read is a RESEQUENCE of a previously sequenced human clone
Original clone citation: WashU-NCI human EST Project
This read has been verified (found to hit its original self in the
correct orientation)
Seq primer: -40UP from Gibco
High quality sequence stop: 449.
FEATURES
Location/Qualifiers
1..484
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:840359"
/sex="male"
/dev_stage="72 years"
/lab_host="SOLR cells (kanamycin resistant)"
/clone_lib="Stratagene lung (#937210)"
/note="Organ: lung; Vector: pBluescript SK-; Site 1:
EcoRI; Site 2: XhoI; Cloned unidirectionally. Primer:
Oligo dT, normal lung. Average insert size: 1.0 kb;
Uni-ZAP XR Vector; -5' adaptor sequence: 5' GAATTCGGCAGG
3' -3' adaptor sequence: 5' CTCGAGTTTTTTTTTTTTTT 3'"

ORIGIN
Query Match 19.3%; Score 226.8; DB 9; Length 484;
Best Local Similarity 77.8%; Pred. No. 1.7e-36;
Matches 273; Conservative 0; Mismatches 78; Indels 0; Gaps 0;
QY 505 TTATTTTATTTCTTTTAGACAGAGTCTCACTCTGTCCACCGCTGGAGTGCAGTGGT 564
Db 455 TTTTGTGTTTCTTTTCAGACAGAGTCTGTCTGTCTACNCAGGCTGGAGAACAGTGGC 396

QY 565 GCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGGATTTCTCATGCCTCCACC 624
Db 395 GTGATCTCGGCTCACTGCAACCTCCACCTCCAGGTTCAAGGATTTCTCCTGCCTCAACC 336
QY 625 TCCCAAGTAGCTGGGACTACAGGCATGACCAACAATGCCCAACTAAATTTTGTATTTTA 684
Db 335 TCCCGAGTAGCTGGGACTACAGGCATGCATCATGAGACCTGGCTAATTTTGTATTTTA 276
QY 685 GTAGAGACGGGTTTTTGCCATGTTGCCAGGCTGGCCTTGAACTCCTGGCCTCAACAAT 744
Db 275 GTAGAAATGGAGTTTGTCTATGTTGGCCAGGCTGGTCTCAAACTCCTGACCTCAAGTGAT 216
QY 745 CCACCTGCCTCGGCCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCCT 804
Db 215 CCACCTGCCTCGGCCTCCCAAAGTGTGGGATTAGAGCTGTGAGCCACTGCACCTGGCCT 156
QY 805 AAACATTATCTTTTCTTTGTGTGGGAACCTTTGAAATTTATACAATGAATT 855
Db 155 ATACTGTCAATTTTAAATAAAATTTAAATATTACATGGCTCAATAAGT 105

RESULT 39
BG335756/c
LOCUS
DEFINITION
BG335756 946 bp mRNA linear EST 27-FEB-2001
602404452F1 NIH_MGC_21 Homo sapiens cDNA clone IMAGE:4542013 5',
mRNA sequence.
ACCESSION
BG335756
VERSION
BG335756.1 GI:13142206
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
REFERENCE
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 946)
AUTHORS
NIH-MGC <http://mgc.nci.nih.gov/>.
TITLE
National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL
Unpublished (1999)
COMMENT
Contact: Robert Strausberg, Ph.D.
Email: cgaps-r@mail.nih.gov
Tissue Procurement: ATCC
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
<http://image.llnl.gov>
Plate: LLC1221 row: h column: 14
High quality sequence stop: 562.
FEATURES
Location/Qualifiers
1..946
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:4542013"
/tissue_type="choriocarcinoma"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIH_MGC_21"
/note="Organ: placenta; Vector: pOTB7; Site 1: XhoI;
Site 2: EcoRI; CDNA made by oligo-dT priming.
Directionally cloned into EcoRI/XhoI sites using the
following 5' adaptor: GGCACGAG(G). Size-selected >500bp
for average insert size 1.8kb. Library constructed by
Ling Hong in the laboratory of Gerald M. Rubin (University
of California, Berkeley) using ZAP-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)."

ORIGIN
Query Match 19.3%; Score 226.8; DB 12; Length 946;
Best Local Similarity 78.9%; Pred. No. 1.6e-36;
Matches 270; Conservative 0; Mismatches 72; Indels 0; Gaps 0;
QY 504 TTTATTTTATTTCTTTTAGACAGAGTCTCACTCTGTCCACCGCTGGAGTGCAGTGG 563

Db	530	TGTTTTTCTTTTTTTTGAGACAGGATCTCACTCTGTGTCA	CCCCAGGCTGGAGTGAATGG	471	
QY	564	TGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATG	CCTCCAC	623	
Db	470	CATGATCTTGACTCACTGCTACCTCCGCTCCAGGTTCAAGTGATTCTCCTG	CTCAGC	411	
QY	624	CTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTG	TATTTTT	683	
Db	410	CTCCCAAGTAGCTGGGACTACAGGCGTGCAACCACCATGCCCGGCTAATTTTG	TATTTTT	351	
QY	684	AGTAGACACGGGGTTTTTGCCATGTTGCCAGGCTGGCCTTGAACTCCTGGCC	CTCAACAA	743	
Db	350	AGCAGACACGGGGTTTCATCATGTTGGCCAGACTGGTCTCGAACTCCTGAC	CTCAGGTGA	291	
QY	744	TCCACTTGCCTCGGCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTG	CGCTGGCC	803	
Db	290	TCTGCTGCCTCAGCCTCCCAAAGTGTGGAAATTACAGGCGTAAGCCACCG	GTGCCCGGC	231	
QY	804	TAAACATTTATCTTTTCTTTTGTGTGGGAACCTTTGAAATTAT	845		
Db	230	TAAAAA	CTTTTAAATGTATACTTTAGTTGGTGAAATTAT	189	
RESULT 40					
BX489032					
LOCUS					
DEFINITION					
ACCESSION					
VERSION					
KEYWORDS					
SOURCE					
ORGANISM					
REFERENCE					
AUTHORS					
TITLE					
JOURNAL					
COMMENT					
FEATURES					
source					
ORIGIN					
Query Match					
Best Local Similarity					
Matches					
QY	504	TTTATTTTCTTTTATCTTTTATGACAGAGTCTCACTCTGTCA	CCCCAGGCTGGAGTGCAGTGG	563	
Db	30	TTTTTCTTTT	TTTTTTGAGACAGAGTCTCGCTCTGTCA	CCCCAGGCTGGAGTGCAGTGG	89

QY	564	TGCCATCTCAGCTTACTGCAACCTCTGCTGCCAGGTTCAAGCGATTCTCATGCTCCAC	623
Db	90	CGCGATCTCGGCTCACTGCAAACTCCACCTCCCGGTTCAAGCAGTTCTCCTGCTCAGC	149
QY	624	CTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTGTATTTT	683
Db	150	CTCCCAAGTAGCTGGGATTACAGGCGTCCGCCACCATGCCAGCCAATTTTGTACTTTT	209
QY	684	AGTAGAGACGGGGTTTTTGCCATGTTGCCAGGCTGGCCTTGAACTCCTGGCCTCAACAA	743
Db	210	AGTAGAGATGGGGTTTACCCATGTTGGCCAGGCTGGTCTCGAACTCCTGACCTCAGGTGA	269
QY	744	TCCACTTGCCTCGGCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGGCC	803
Db	270	TCCACTCGCCTCGGCTCCCAAAGTGTGGGATTATAGGCATGCCGCCACCATGCCCGGCC	329
QY	804	TAAACATTTATCTTTTCTTTGTTGGGAACCTTTGAAATTATACAATGAATTATTGTTAA	863
Db	330	GGCTTATGATTTAAACATGAATGTTTATTCTTGGAATTTCCACATAATATTTTGTGA	389
QY	864	C	864
Db	390	C	390
RESULT 41			
CB296753			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			
ORGANISM			
REFERENCE			
AUTHORS			
TITLE			
JOURNAL			
COMMENT			
FEATURES			
source			
ORIGIN			
Query Match			
Best Local Similarity			
Query Match			
Best Local Similarity			


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Matches 256; Conservative 0; Mismatches 49; Indels 0; Gaps 0;
QY 504 TTTATTTTATTTATTTTATTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGG 563
Db 41 TTCACCTTTTATTTTATTTTATTTGAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCATGG 100
QY 564 TGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCAC 623
Db 101 CATCATCTCGGCTCACTGCAACCTCTGCCTCCAGGTTCAAGTGATTCTCCTGCCCTCAGC 160
QY 624 CTCCCAAGTAGCTGGGACTACAGGCATGACCCACACAATGCCCAACTAATTTTGTATTTT 683
Db 161 CTCTCGAGTAGCTGGGACTGCAGGCATGTACCACTCTGCCAGCTAATTTTCATATTTT 220
QY 684 AGTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGCCCTTGAATCTCCTGGCTCAACAA 743
Db 221 AGTAGAGACGGGGTTTTCATCTTGTGGCCAGGCTGGTCTCAAACTCCTGACATCAAGTGA 280
QY 744 TCCACTTGCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCCTGCC 803
Db 281 TCCGCCTGCCTTGGCTTCCCAAGCGCTGGGATTACAGGCGTGAGCCACCGCGCCGCC 340
QY 804 TAAAC 808
Db 341 TGAAC 345
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```
RESULT 42
AG178621/c
LOCUS
DEFINITION
  Pan troglodytes DNA, clone: RP43-050K09.TJ, genomic survey
  sequence.
ACCESSION
  AG178621
VERSION
  AG178621.1 GI:16708301
KEYWORDS
  GSS.
SOURCE
  Pan troglodytes (chimpanzee)
ORGANISM
  Pan troglodytes
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
  1
  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
  Totoki,Y., Watanabe,H. and Sakaki,Y:
  BAC end sequences of Library RPCI-43
  Unpublished
  2 (bases 1 to 676)
  Fujiyama,A., Hattori,M., Toyoda,A., Taylor,T.D., Yada,T.,
  Totoki,Y., Watanabe,H. and Sakaki,Y.
  Direct Submission
  Submitted (02-AUG-2001) Asao Fujiyama, The Institute of Physical
  and Chemical Research (RIKEN), Genomic Sciences Center (GSC);
  1-7-22 Suehiro-chou,Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan
  (E-mail:chimbesc@psc.riken.go.jp, URL:http://hgp.gsc.riken.go.jp/,
  Tel:81-45-503-9111, Fax:81-45-503-9170)
  Clones are derived from the chimpanzee BAC library RPCI-43 This BAC
  end was generated during the R&D process and may have higher chance
  of clone tracking errors.
  PRIMERS
  Sequencing: TJ
  LIBRARY
  Vector : pBACe3.6
  R.Site 1 : EcoRI
  R.Site 2 : EcoRI.
  Location/Qualifiers
    1..676
      /organism="Pan troglodytes"
      /mol_type="genomic DNA"
      /db_xref="taxon:9598"
      /clone="RP43-050K09.TJ"
      /sex="male"
      /cell_type="lymphocytes"
      /clone_lib="RPCI-43 Chimpanzee Male BAC Library"
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FEATURES

source

ORIGIN

```
Query Match 19.3%; Score 226.6; DB 29; Length 676;
Best Local Similarity 82.7%; Pred. No. 1.8e-36;
Matches 259; Conservative 0; Mismatches 54; Indels 0; Gaps 0;
QY 505 TTATTTTATTTATTTTATTTAGACAGAGTCTCACTCTGTCAACCAGGCTGGAGTGCAGTGGT 564
Db 406 TTGTTGTTGTTGTTATTTAGACAGAGTCTCACTCTGTGCCAGGCTGGAGTGCATGGC 347
QY 565 GCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCCCTCCACC 624
Db 346 GCAATCTCGGCTCACTGCAACCTCTGCCTCCGGGCTCAAGTGATTCTCCTGCCCTCAGCC 287
QY 625 TCCCAAGTAGCTGGGACTACAGGCATGACCCACACAATGCCCAACTAATTTTGTATTTTA 684
Db 286 TCCTGAGTAGCTAGGTTACAGGCACGCACCAACCAACGCTAATTTTGTATTTTA 227
QY 685 GTAGAGACGGGGTTTGGCCATGTTGCCAGGCTGGCCCTTGAATCTCCTGGCTCAACAAAT 744
Db 226 GTAGAGACGGGGTTTACCATGTTGCCAGGCTGGTCTTGAATCTCCTGACCTCAGGTGAT 167
QY 745 CCACCTTGCCTCGGCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCCTGCCCT 804
Db 166 CCACCCGCTCAGCCTCCCAAGTGTGGGTTTACAGGCGTGAGCCGCTGCCCTGGCTT 107
QY 805 AAACATTTATCTT 817
Db 106 ACAGGGTTTTTTT 94
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```
RESULT 43
AQ543621/c
LOCUS
DEFINITION
  RPCI-11-346H5.TV RPCI-11 Homo sapiens genomic clone RPCI-11-346H5,
  genomic survey sequence.
ACCESSION
  AQ543621
VERSION
  AQ543621.1 GI:4873905
KEYWORDS
  GSS.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 681)
  Zhao,S., Adams,M.D., Nierman,W., Malek,J., de Jong,P. and
  Venter,J.C.
  Use of BAC End Sequences from Library RPCI-11 for Sequence-Ready
  Map Building
  Unpublished (1997)
  Other_GSSs: RPCI-11-346H5.TJ
  Contact: Shaying Zhao, William Nierman, Mark Adams
  Department of Eukaryotic Genomics
  The Institute for Genomic Research
  9712 Medical Center Dr., Rockville, MD 20850
  Tel: 301 838 0200
  Fax: 301 838 0208
  Email: hbe@tigr.org
```

Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering) or from Research Genet cs (info@resgen.com). BAC end search page: http://www.tigr.org/tdb/hungen/bac_end_search/bac_end_search.html.

Seq primer: T7

Class: BAC ends.
Location/Qualifiers
1..681
/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="GDB:7632652"
/db_xref="taxon:9606"
/clone="RPCI-11-346H5"
/sex="Male"
/cell_type="Lymphocytes"
/clone_lib="RPCI-11"

FEATURES

source

```
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;  
RPCI11 Human Male BAC Library"
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ORIGIN

Query Match	19.3%;	Score 226.6;	DB 28;	Length 681;
Best Local Similarity	82.7%;	Pred. No. 1.8e-36;		
Matches 259;	Conservative 0;	Mismatches 54;	Indels 0;	Gaps 0;
QY	504	TTTATTTTTTAACTCTTTT	TAGACAGAGTCTCACTCTGTCA	CCCGAGGCTGGAGTGCAGTGG 563
Db	323	TTTTTTTTTTTTTTTTTTTT	TGAGACAGAGTCTCACTCTGTGG	CCCGAGGCTGGAGTGCAGTGG 264
QY	564	TGCCATCTCAGCTTACTGCA	ACCTCTGCCTGCCAGGTTCAAG	CGATTCTCATGCGCTCCAC 623
Db	263	TGCGATCTCAGCTCACTGCA	ACCTCCGCCCTCCAGGTTCAAG	TGATTCTCCTCGCCTTAGC 204
QY	624	CTCCCAAGTAGCTGGGACT	TACAGGCATGCACCACAATGC	CCCACTAATTTTGTATTTT 683
Db	203	CTCCCAAGTAGCTGGGATT	TATAGGTGTCACCACCACAC	ACAGCTAATTTTGTGTTTT 144
QY	684	AGTAGAGACGGGGTTTTTG	CCCATGTTGCCCGAGGCTGG	CCTTGAACCTCGCCCTCAACAA 743
Db	143	AGTAGAGACAGGGTTTCA	CCCATGTTGGCCAGGCTGGT	CTCAAACTCCTGACCTCAGGTCA 84
QY	744	TCCACTTGCCTCGGCCTCC	CAAGTGTATGATTACAGCGGT	GAGCCACCGTGCCCTGGCC 803
Db	83	TCCTCCACCTTGGCCTCC	CAAGTGTGCGAATTACAGCG	GGGAGCCACTGCGCCTGGCC 24
QY	804	TAAACATTTATCT		816
Db	23	TATAGCTGAATTT		11

RESULT 44

BI752166
LOCUS
DEFINITION
BI752166 712 bp mRNA linear EST 25-SEP-2001
60302224F1 NIH_MGC_114 Homo sapiens cDNA clone IMAGE:5192867 5',
mRNA sequence.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 712)
NIH-MGC <http://mgc.nci.nih.gov/>.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.

FEATURES
SOURCE

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/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5192867"
/lab_host="DH10B"
/clone_lib="NIH_MGC_114"
/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: EcoRV (destroyed); RNA source anonymous pool of 6
male brains, age range 23-27 yo. Library is oligo-dT
primed and directionally cloned (EcoRV site is destroyed
upon cloning). Average insert size 1.5 kb, insert size

```

range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 019. Note: this is a NIH MGC Library."

ORIGIN

Query Match	19.3%;	Score 226.6;	DB 12;	Length 712;
Best Local Similarity	78.6%;	Pred. No. 1.8e-36;		
Matches 271; Conservative	0;	Mismatches 74;	Indels 0;	Gaps 0;

Qy	492	TCACATCAAAACATTATTTTATTTCTTTTAGACAGAGTCTCACTCTGTCCACCAGGCT	551
Db	100	TTAATTCATTATTTTATTTTATTTTGGACAGAGTCTCACCTCTGTCTCATCTAGGCT	159
Qy	552	GGAGTGCGAGTGGTGCCATCTCAGCTTACTGCAACCTCTGCCTGCCAGGTTCAAAGCGATT	611
Db	160	GGAGTGCGAGTGGTGCAATCTTGGCTTGCTGAATCTCCACCTCCCAGGTTCAAAGCGATT	219
Qy	612	TCATGCCTCCACCTCCCCAAGTAGCTGGACTACAGGCATGCACCACAATGCCCACTAAT	671
Db	220	TCCCACTTCAGCCTCCCGAGTAGCTGGATTACAGGCATGCGCCACCATGCCCTGGCTAAT	279
Qy	672	TTTTGTATTTTAGTAGAGACGGGGTTTTGCCCATGTTGCCCAGGCTGGCCTTGAACCTCCT	731
Db	280	TTTTGTATTTTAGTAGAGACGGGGTTTCGCCATGTTGGCCAGGCTCGTCTCGAACCTCCT	339
Qy	732	GGCCTCAAAACAATCCACTTGCCCTCGGCCCTCCAAAAGTGTTATGATTACAGCGTGCAGCCA	791
Db	340	GGCCTCAAGTGATCTGCCCGCCTCAGCCTCCCAAAAGTGCTGGGATTACAATATGAGCTA	399
Qy	792	CCGTGCCTGGCCTAAACATTTATCTTTCTTTGTGTGGGAACCTT	836
Db	400	CTATGCTGGTCCCAACTTCTTAAAAATTAPAACTTTTCGGGGAAGTT	444

RESULT 45

CK005530
LOCUS CK005530 631 bp mRNA linear EST 26-NOV-2003
DEFINITION AGENCOURT 16386158 NIH MGC 229 Homo sapiens cDNA clone
IMAGE:30721940 5', mRNA sequence.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 631)
 NIH-MGC <http://mgc.ncbi.nlm.nih.gov/>.
 National Institutes of Health, Mammalian Gene Collection (MGC)
 Unpublished (1999)
 Contact: Daniela S. Gerhard, Ph.D.

FEATURES
source

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 813)
Volik,S., Zhao,S., Chin,K., Brebner,J.H., Herndon,D.R., Tao,Q., Kowbel,D., Huang,G., Lapuk,A., Kuo,W.-L., Magrane,G., de Jong,P., Gray,J.W. and Collins,C.
End-sequence profiling: Sequence-based analysis of aberrant genomes
Proc. Natl. Acad. Sci. U.S.A. 100 (13), 7696-7701 (2003)
22709111
12788976
Contact: Volik SV
Colin Collins' lab
UCSF Comprehensive Cancer Center
UCSF Box 0808, San Francisco, CA 94143-0808, USA
Tel: 415 502 7066
Fax: 415 502 5665
Email: svolik@cc.ucsf.edu
This clone is available from Amplicon Express
http://www.genomex.com
Class: BAC ends.

FEATURES
source
1. .813
/organism="Homo sapiens"
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/db_xref="taxon:9606"
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/note="Vector: pEBCAC1; Site 1: HindIII; This library was constructed from MCF7 breast cancer cell line by Amplicon Express (http://www.genomex.com) using their standard procedure."

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Query Match 19.2%; Score 226.4; DB 28; Length 813;
Best Local Similarity 63.4%; Pred. No. 1.9e-36;
Matches 425; Conservative 0; Mismatches 216; Indels 29; Gaps 4;
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667 TTTATGTTTGGCTTTTGAGACAGAGT----CTCTCTACCCAGGCTGGAGTGCAGTGG 612
564 TGCCATCTCAGCTTACTGCAACCTCTGCCT-GCCAGGTTCAAGCGATTCTCATGCCTCCA 622
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611 CACGATCTCAGCCCACTGCAACCTCCACCTCCCCAAGCTGAAGTGATTCTCCIGCTCAG 552
623 CCTCCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTGTATTTT 682
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551 CCTCCTCAGTAGCTGGGACTACAGGTGCGCACCCACCACGCCCTGCTAATTTTGTATTTT 492
683 TAGTAGACACGGGGTTTGGCATGTTGCCATGTTGCCAGGCTGCCCTGAACCTCCTGGCCTCAAACA 742
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491 TAGTAGAGACTGGGTTTCACTATGTTGGCCAGGCTGGTCTTGAACCTCCTGACCTCAGGTG 432
743 ATCCACTTGCCTCGGCCCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGC 802
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431 ATCCACCTGCCTCAGCCTCCCAAGTGTAGGATTGCAGGCATGAGCCACTGTGCCCAGC 372
803 CTAAACAATTATCTTTTCTT-----TGTGTTGGGAACCTTTGAAATTATACAATG 851
371 CATGTTTTCGCTTTTAAATTGGTGGTAAATAATACATAACAACAATTACCATCTTAACCAT 312
852 AATTATTGTTAACTGTTCATCTCCCTGTGTGCTATGGAACACTGGGACTTCTTCCCTCTA 911
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311 TTTTAAATGACGCTTTTGTAGTATTGAGTTCATACATATTATTGTGCAACCAATCTTGAG 252
912 TCTAACTGTATATTGTACCAGTTAACCACCGTACTTTCATCTCCCACTCCTCTCTATCCT 971
|||||
251 AACTCTTTTCGCTTTCGCAAACTGAACTCTGTTCCTTTAAATGACAAATCCCTATTC 192
972 TCCCAACCTCTGTATCACCTCA-----TTCTACTCTCTACCTCCATGAGATCC 1018
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Db 191 TCAACTCTGCCAAGCAGCTTGGATTAGAACTACTTTTCTACTTTCTGTCTCTATGAGTTTA 132
QY 1019 ACTTTTGTAGCTCCACATGTGAGTAAGAAAAATGCAATATTGTCTTTCTGTGCCTGGCT 1078
|||||
Db 131 ACTACTCTAGGTTCTCTCATGTATGTGGAATCATACAGTATTGTCTTTTCATGACTGGCT 72
1079 TATTTCACTTAACATAATGACTTCTCTGTTCATCCATGTTGTCGCAAAATGACAGGATTC 1138
|||||
Db 71 TATTTCACTTAGTATAATGTCCCGAGGTTTCATCCATGTTGTAGCATGTATTAGAATTC 12
QY 1139 GTTCTTAATT 1148
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Db 11 CTTCCTTTT 2

RESULT 48
AQ747273/c
LOCUS
DEFINITION
genomic clone Plate=1113 Col=21 Row=K, genomic survey sequence.
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 928)
Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T.,
Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and
Hood,L.
Sequence-tagged connectors: A sequence approach to mapping and
scanning the human genome
Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)
99380589
10449764
Contact: Mahairas GG, Wallace JC, Hood L
High Throughput Sequencing Center
University of Washington
401 Queen Anne Avenue North, Seattle, WA 98109, USA
Tel: (206) 616-3618
Fax: (206) 616-3887
Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC
library availability, please contact Pieter de Jong
(pieter@dejong.med.buffalo.edu). Clones may be purchased from
BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm)
or from Resear h Genetics (info@resgen.com). BAC end Web Server:
http://www.htsc.washington.edu
Plate: 1113 row: K column: 21
Seq primer: T7
Class: BAC ends
High quality sequence stop: 928.
Location/Qualifiers
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/sex="male"
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/note="Vector: pBACE3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACE3.6 vector at EcoRI sites"

ORIGIN
Query Match 19.2%; Score 226.4; DB 28; Length 928;
Best Local Similarity 76.4%; Pred. No. 1.9e-36;
Matches 278; Conservative 0; Mismatches 86; Indels 0; Gaps 0;
QY 478 AACTGGGATATCCATCACATCAAAACATTATTTTATTCTTTTAGACAGAGTCTCACT 537

[illegible]

RESULT	49
AQ745166/c	
LOCUS	
DEFINITION	
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AQ745166	784 bp
HS_5502_A2_C07_SP6_RPCI-11	DNA linear
genomic_clone_Plate=1078	Human Male BAC Library Homo sapiens
Col=14	Row=E, genomic survey sequence.
GSS	16-JUL-1999

FEATURES	SOURCE
1. <u>Age</u>	1. <u>Age</u>
2. <u>Gender</u>	2. <u>Gender</u>
3. <u>Marital Status</u>	3. <u>Marital Status</u>
4. <u>Education</u>	4. <u>Education</u>
5. <u>Income</u>	5. <u>Income</u>
6. <u>Occupation</u>	6. <u>Occupation</u>
7. <u>Religion</u>	7. <u>Religion</u>
8. <u>Political Affiliation</u>	8. <u>Political Affiliation</u>
9. <u>Health Status</u>	9. <u>Health Status</u>
10. <u>Travel History</u>	10. <u>Travel History</u>
11. <u>Employment Status</u>	11. <u>Employment Status</u>
12. <u>Family Size</u>	12. <u>Family Size</u>
13. <u>Home Ownership</u>	13. <u>Home Ownership</u>
14. <u>Vehicle Ownership</u>	14. <u>Vehicle Ownership</u>
15. <u>Insurance Status</u>	15. <u>Insurance Status</u>
16. <u>Substance Use</u>	16. <u>Substance Use</u>
17. <u>Mental Health</u>	17. <u>Mental Health</u>
18. <u>Chronic Conditions</u>	18. <u>Chronic Conditions</u>
19. <u>Vaccination Status</u>	19. <u>Vaccination Status</u>
20. <u>Compliance with Health Guidelines</u>	20. <u>Compliance with Health Guidelines</u>

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/clone lib="RPCI-11 Human Male BAC Library"  
/note="Vector: pBACe3.6; Site_1: EcoRI; Site_2: EcoRI;  
Male blood DNA was isolated from one randomly chosen donor  
and partially digested with a combination of EcoRI and  
EcoRI Methylase. Size selected DNA was cloned into the  
pBACe3.6 vector at EcoRI sites"
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ORIGIN

Query Match	19.2%;	Score 226.2;	DB 28;	Length 784;	
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Matches 261;	Conservative	0;	Mismatches 58;	Indels 0;	Gaps 0;
QY	505	TTATTTTATCTCTTTTAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGT	564		
Db	331	TTTTTTTTTTTTTCTTTTGAGACAGAGTCTCACTCTGTCACCCAGGCTGGAGTGCAGTGGC	272		
QY	565	GCCATCTCAGCTTACTGCAACCTCTGCCCTGCCAGGTTCAAGCGATTCTCATGCCTCCACC	624		
Db	271	TCGATCTCAGCTCACTCCAACCTCTGCCCTCCGGGATTCGAAGTGATCTCCAGCCTCAGCC	212		
QY	625	TCCAAGTAGCTGGGACTACAGGCATGCACCACAATGCCCAACTAATTTTGTATTTTA	684		
Db	211	TCCAAGTAGCTGGAAATTATAGCAAGTGCCACCATTGCCCGGCTAATTTTGTATTTTA	152		
QY	685	GTAGACACGGGGTTTTGGCATGTTGCCCATGTTGCCCAGGCTGGCCCTTGAACCTCCTGGCCTCAAAACAAT	744		
Db	151	GTAGACACAGGGTTTTGGCATCCTGGCCAGGCTGGTCTCGAACTCCTGGCCTCAAGTAAT	92		
QY	745	CCACTTGCCTCGGCCCTCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCCT	804		
Db	91	CTGCGCTGCTTCGGCCTCTCAAAGTGTGGGATTACAGGCATGAGCCATTGTGCCCGACCC	32		
QY	805	AAACATTTATCTTTTCTTT	823		
Db	31	CAATTTTTTCTTTTACTTT	13		

RESULT 50	828 bp	DNA	linear	GSS 19-JUL-1999
AQ749749				
LOCUS				
DEFINITION	HS_5573_A2_C02_T7A RPCI-11 Human Male BAC Library Homo sapiens			
	genomic_clone_Plate=1149 Col=4 Row=E, genomic survey sequence.			
ACCESSION	AQ749749			
VERSION	AQ749749.1	GI:5536907		
KEYWORDS	GSS.			
SOURCE	Homo sapiens (human)			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
REFERENCE	1 (bases 1 to 828)			
AUTHORS	Mahairas,G.G., Wallace,J.C., Smith,K., Swartzell,S., Holzman,T., Keller,A., Shaker,R., Furlong,J., Young,J., Zhao,S., Adams,M.D. and Hood,L.			
TITLE	Sequence-tagged connectors: A sequence approach to mapping and scanning the human genome			
JOURNAL	Proc. Natl. Acad. Sci. U.S.A. 96 (17), 9739-9744 (1999)			
MEDLINE	99380589			
PUBMED	10449764			
COMMENT	Contact: Mahairas GG, Wallace JC, Hood L High Throughput Sequencing Center University of Washington 401 Queen Anne Avenue North, Seattle, WA 98109, USA Tel: (206) 616-3618 Fax: (206) 616-3887 Email: jwallace@u.washington.edu Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (http://bacpac.med.buffalo.edu/ordering_bac.htm) or from Resear h Genetics (info@resgen.com). BAC end Web Server: http://www.htsc.washington.edu Plate: 1149 row: E column: 4 Seq primer: T7			

Email: jwallace@u.washington.edu
Clones are derived from the human BAC library RPCI-11. For BAC library availability, please contact Pieter de Jong (pieter@dejong.med.buffalo.edu). Clones may be purchased from BACPAC Resources (<http://bacpac.med.buffalo.edu/ordering/bac.htm>) or from Research Genetics (info@resgen.com). BAC end Web Server: <http://www.htsc.washington.edu>
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Seq primer: SP6
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High quality sequence stop: 784.
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/note="vector: pBACe3.6; Site 1: EcoRI; Site 2: EcoRI;
Male blood DNA was isolated from one randomly chosen donor
and partially digested with a combination of EcoRI and
EcoRI Methylase. Size selected DNA was cloned into the
pBACe3.6 vector at EcoRI sites"

ORIGIN

Query Match	19.2%;	Score 226.2;	DB 28;	Length 828;		
Best Local Similarity	81.8%;	Pred. No. 2.1e-36;				
Matches 261;	Conservative 0;	Mismatches 58;	Indels 0;	Gaps 0;		
QY	504	TTTATTTT	TATTTT	TAGACAGAGTCTC	ACTCTGTCACCCAGGCTGGAGTGCAGTGG	563
Db	336	TTTTTTTT	TTTTTT	TGAGACAGAGTCTC	ATTTCTGTCACCTAGGCTGGAGTGCAGTGG	395
QY	564	TGCCATCTCAGCTT	ACTGCAACCTCTGCCTGCGAGGTT	CAAGCGATTCTCATGCGCTCCAC	623	
Db	396	CATGGTCTCGGCTC	ACTGCAACCTCCGCCTCCTGGGTT	CAGGCGATTCTCTTGCCTCAGC	455	
QY	624	CTCCCAAGTAGCTGGG	ACTACAGGCAATGCACACAATGCCCAACTAATTTTGTATTTT	683		
Db	456	CTCCCAAGTAGCTGGG	ATTACAGGCAACACACCACCGCCAGCTAATTTTGTATTTT	515		
QY	684	AGTAGAGACGGGGT	TTTGCCATGTTGCCCAGGCTGGCCTTGAACCTCCTGGCCTCAAA	743		
Db	516	AGTAGAGATGGGGT	TTTGCCCTGTTAGCCAGGCTAGTCTTGAACCTCCTGACCTCAGGTGA	575		
QY	744	TCCACTTGCCTCGGCCT	CCCCAAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCC	803		
Db	576	TCCACTTGCCTCGGCCT	TCCAAAGTGTCTGGGATTACAGGTTTGAGTCACCCACGCCCGCC	635		
QY	804	TAAACATTTATCTTTT	TCTT	822		
Db	636	AGCATTTTGAGATTTT	TCTT	654		

Search completed: September 16, 2004, 21:02:02
Job time : 2928 secs

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM nucleic - nucleic search, using sw model

Run on: September 16, 2004, 17:43:13 ; Search time 4560 Seconds
(without alignments)
11187.445 Million cell updates/sec

Title: US-10-063-736-129
Perfect score: 1177
Sequence: 1 aacttctacatgggcctcct.....ataaccacacatggcaaaaa 1177

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0
Searched: 3470272 seqs, 21671516995 residues 6940544
Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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3:	gb	in:	*		3:	gb	in:	*	
4:	gb	om:	*		4:	gb	om:	*	
5:	gb	ov:	*		5:	gb	ov:	*	
6:	gb	pat:	*		6:	gb	pat:	*	
7:	gb	ph:	*		7:	gb	ph:	*	
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12:	gb	sy:	*		12:	gb	sy:	*	
13:	gb	un:	*		13:	gb	un:	*	
14:	gb	vi:	*		14:	gb	vi:	*	
15:	em	ba:	*		15:	em	ba:	*	
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18:	em	in:	*		18:	em	in:	*	
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21:	em	or:	*		21:	em	or:	*	
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41:	em	htgo_other:	*		41:	em	htgo_other:	*	

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB	ID	Description
1	1177	100.0	1177	6	AX092398	AX092398 Sequence
2	1177	100.0	1177	6	AX358958	AX358958 Sequence
3	1177	100.0	1177	6	AX362451	AX362451 Sequence
4	1177	100.0	1177	6	AX376314	AX376314 Sequence
5	1177	100.0	1177	6	AX454686	AX454686 Sequence
6	1177	100.0	1177	6	AX491164	AX491164 Sequence
7	1177	100.0	1177	9	AY358613	AY358613 Homo sapi
8	1173.4	99.7	159272	9	HSDJ686C3	AL049712 Human DNA
9	1059.8	90.0	2560	6	AX833218	AX833218 Sequence
10	1059.8	90.0	2560	9	AK094789	AK094789 Homo sapi
11	800	68.0	801	6	BD222657	BD222657 Human sig
12	428	36.4	3566	9	AK127751	AK127751 Homo sapi
13	370.6	31.5	162023	9	AC084033	AC084033 Homo sapi
14	370.6	31.5	168283	2	AC027633	AC027633 Homo sapi
15	351.8	29.9	162145	9	AC131572	AC131572 Homo sapi
16	351	29.8	136124	9	HS394P21	AL021528 Human DNA
17	350.2	29.8	151068	9	AL133405	AL133405 Human DNA
18	349.8	29.7	91503	9	AL451061	AL451061 Human DNA
19	349.6	29.7	30826	9	AL807743	AL807743 Human DNA
20	349.6	29.7	182408	9	HS4535K18	AL078638 Human DNA
21	347	29.5	150520	9	AL136305	AL136305 Human DNA
22	346.4	29.4	176222	9	AC011825	AC011825 Homo sapi
23	345.4	29.3	147569	2	BX248417	BX248417 Homo sapi
24	345.4	29.3	155112	2	AL357521	AL357521 Homo sapi
25	345.4	29.3	158297	2	AL513545	AL513545 Homo sapi
26	344.4	29.3	120099	9	AC011449	AC011449 Homo sapi
27	344.4	29.3	179409	9	AC009831	AC009831 Homo sapi
28	342.6	29.1	160915	2	AP001084	AP001084 Homo sapi
29	342.6	29.1	165420	9	AC091588	AC091588 Homo sapi
30	342.6	29.1	171978	2	AC009669	AC009669 Homo sapi
31	342.6	29.1	204504	2	AC022487	AC022487 Homo sapi
32	342.6	29.1	208310	9	AC091043	AC091043 Homo sapi
33	341.4	29.0	167444	9	AL583862	AL583862 Human DNA
34	337.4	28.7	184541	9	AC011405	AC011405 Homo sapi
35	335.8	28.5	193979	9	AC017078	AC017078 Homo sapi
36	334.8	28.4	196954	9	AC008267	AC008267 Homo sapi
37	334.2	28.4	157017	9	AL162389	AL162389 Human DNA
38	332.8	28.3	107685	9	BX679664	BX679664 Human DNA
39	330.8	28.1	167357	9	CNS01DWY	AL138976 Human chr
40	330.6	28.1	58075	9	AC111197	AC111197 Homo sapi
41	330.4	28.1	156635	9	AC105285	AC105285 Homo sapi
42	330	28.0	142521	2	AC023018	AC023018 Homo sapi
43	330	28.0	175842	9	AL731547	AL731547 Human DNA
44	329.6	28.0	32074	9	AC104533	AC104533 Homo sapi
45	329.4	28.0	140091	9	AL445684	AL445684 Human DNA

ALIGNMENTS

RESULT 1	AX092398	1177 bp	DNA	linear	PAT 21-MAR-2001
AX092398	Sequence 129 from Patent WO0116318.				
LOCUS	AX092398				
DEFINITION	Sequence 129 from Patent WO0116318.				
ACCESSION	AX092398				
VERSION	AX092398.1	GI:13444513			
KEYWORDS	.				
SOURCE	Homo sapiens (human)				
ORGANISM	Homo sapiens				
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
REFERENCE	1				
AUTHORS	Eaton,D.L., Filvaroff,E., Gerritsen,M.E., Goddard,A.,				
	Godowski,P.J., Grimaldi,C.J., Gurney,A.L., Watanabe,C.K. and				
	Wood,W.I.				

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0116318-A 129 08-MAR-2001; Genentech, Inc. (US)

FEATURES Location/Qualifiers

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/organism="Homo sapiens"

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Best Local Similarity 100.0%; Pred. No. 5e-275;

Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX358958 1177 bp DNA linear PAT 13-FEB-2002

DEFINITION Sequence 211 from Patent WO0193983.

ACCESSION AX358958

VERSION AX358958.1 GI:18675380

KEYWORDS

SOURCE Homo sapiens (human)

ORGANISM Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1

AUTHORS Baker, K.P., Desnoyers, L., Gerritsen, M.E., Goddard, A., Godowski, P.J., Grimaldi, J.C., Gurney, A.L., Smith, V., Stephan, J.P., Watanabe, C.K. and Wood, W.I.

TITLE Secreted and transmembrane polypeptides and nucleic acids encoding the same

JOURNAL Patent: WO 0193983-A 211 13-DEC-2001; Genentech Inc. (US)

FEATURES Location/Qualifiers

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Best Local Similarity 100.0%; Pred. No. 5e-275;

Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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LOCUS AX362451 1177 bp DNA linear PAT 15-FEB-2002
DEFINITION Sequence 211 from Patent WO208288.
ACCESSION AX362451
VERSION AX362451.1 GI:18694683
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1

AUTHORS Baker,K.P., Desnoyers,L., Gerritsen,M.E., Goddard,A.,
Godowski,P.J., Grimaldi,J.C., Gurney,A.L., Smith,V., Stephan,J.P.,
Watanabe,C.K. and Wood,W.I.
TITLE Secreted and transmembrane polypeptides and nucleic acids encoding
the same
JOURNAL Patent: WO 0208288-A 211 31-JAN-2002;
Genentech, Inc. (US)
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Best local Similarity 100.0%; Pred. No. Se-275;
Matches 1177; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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VERSION
KEYWORDS
SOURCE
ORGANISM

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AY358613
AY358613.1 GI:37182347
FLI_CDNA.
Homo sapiens (human)

REFERENCE
AUTHORS

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Clark,H.F., Gurney,A.L., Abaya,E., Baker,K., Baldwin,D., Brush,J.,
Chen,J., Chow,B., Chui,C., Crowley,C., Currell,B., Deuel,B.,
Dowd,P., Eaton,D., Foster,J., Grimaldi,C., Gu,Q., Hass,P.E.,
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Stinson,J., Vagts,A., Vandlen,R., Watanabe,C., Wieand,D., Woods,K.,
Xie,M.H., Yatsura,D., Yi,S., Yu,G., Yuan,J., Zhang,M., Zhang,Z.,
Goddard,A., Wood,W.I. and Godowski,P.
The Secreted Protein Discovery Initiative (SPDI), a Large-Scale
Effort to Identify Novel Human Secreted and Transmembrane Proteins:
A Bioinformatics Assessment

TITLE

JOURNAL
PUBMED
REFERENCE
AUTHORS
TITLE
JOURNAL

Genome Res. 13 (10), 2265-2270 (2003)
12975309
2 (bases 1 to 1177)
Clark,H.F.
Direct Submission
Submitted (01-AUG-2003) Department of Bioinformatics, Genentech,
Inc., 1 DNA Way, South San Francisco, CA 94080, USA

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Db	54381		54322
QY	421	GGGGGTACATGTGATATTGGATACATGTATACAATATATAATGATCAAAATCAGGGTAAC	480
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QY	481	TGGGATATCCATCACATCAAAACATTTATTTTATTTCTTTTATAGACAGTCTCACTCTG	540
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DEFINITION	Sequence 342 from Patent EP1347046.	linear	PAT 15-DEC-2003
ACCESSION	AX833218		
VERSION	AX833218.1	GI:39919353	
KEYWORDS			
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens		
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE	1		

AUTHORS	Isogai,T., Sugiyama,T., Otsuki,T., Wakamatsu,A., Sato,H., Ishii,S., Yamamoto,J.I., Isono,Y., Hio,Y., Otsuka,K., Nagai,K., Irie,R., Tamechika,I., Seki,N., Yoshikawa,T., Otsuka,M., Nagahari,K. and Masuho,Y.									
TITLE	Full-length cDNA sequences									
JOURNAL	Patent: EP 1347046-A 342 24-SEP-2003;									
FEATURES	Research Association for Biotechnology (JP)									
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Matches 1061; Conservative	0; Mismatches 2; Indels 0; Gaps 0;									
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LOCUS Homo sapiens cDNA FLJ37470 fis, clone BRAWH2012258.
DEFINITION AK094789
ACCESSION AK094789
VERSION AK094789.1 GI:21753918
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE 1
AUTHORS Suzuki, O., Sasaki, N., Aotsuka, S., Shoji, T., Ichihara, T., Shiohata, N., Matsumoto, K., Hirano, M., Sano, S., Nomura, R., Yoshikawa, Y., Matsumura, Y., Moriya, S., Chiba, E., Momiyama, H., Onogawa, S., Kaeriyama, S., Satch, N., Matsunawa, H., Takahashi, E., Kataoka, R., Kuga, N., Kuroda, A., Satoh, I., Kamata, K., Takami, S., Terashima, Y., Watanabe, M., Sugiyama, T., Irie, R., Otsuki, T., Sato, H., Ota, T., Wakamatsu, A., Ishii, S., Yamamoto, J., Isono, Y., Kawai-Hio, Y., Saito, K., Nishikawa, T., Kimura, K., Yamashita, H., Matsuo, K., Nakamura, Y., Sekine, M., Kikuchi, H., Kanda, K., Wagatsuma, M., Murakawa, K., Kanehori, K., Takahashi-Fujii, A., Oshima, A., Sugiyama, A., Kawakami, B., Suzuki, Y., Sugano, S., Nagahari, K., Masuho, Y., Nagai, K. and Isogai, T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 2560)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 2560)
Isogai, T. and Yamamoto, J.
Direct Submission
Submitted (04-JUL-2002) Takao Isogai, FLJ Project (HRI Team); 2-6-7 Kazusa-Kamatari, Kisarazu, Chiba 292-0812, Japan
(E-mail: genomics@hri.co.jp, Tel: 81-438-52-3975, Fax: 81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing: Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.
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FEATURES
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Best Local Similarity 99.8%; Pred. No. 1.5e-246;
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LOCUS Human signal peptide-containing protein.
DEFINITION
ACCESSION BD222657
VERSION BD222657.1 GI:33032427
KEYWORDS JP 2002519030-A/3.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 801)
AUTHORS Lal,P., Tang,Y.T., Gorgone,G.A., Corley,N.C., Guegler,K.J.,
Baughn,M.R., Akerblom,I.E., Young,J.A., Yue,H., Patterson,C.,
Reddy,R., Hillman,J.L. and Bandman,O.
TITLE Human signal peptide-containing protein
JOURNAL Patent: JP 2002519030-A 3 02-JUL-2002;
INCYTE PHARMACEUTICALS INC
COMMENT OS Homo sapiens (human)
PN JP 2002519030-A/3
PD 02-JUL-2002
PF 25-JUN-1999 JP 2000557363
PR 26-JUN-1998 US 60/090762,31-JUL-1998 US 60/094983 PR
01-OCT-1998 US 60/102686,11-DEC-1998 US 60/112129 PI PREETI
LAL,Y TOM TANG,GINA A GORGONE,NEIL C CORLEY,KARL J PI GUEGLER,
PI MARIAH R BAUGHN,INGRID E AKERBLOM,JANICE AU YOUNG,HENRY YUE,
PI CHANDRA PATTERSON,ROOPA REDDY,JENNIFER L HILLMAN,OLGA BANDMAN
PC C12N15/09,A61K38/00,A61K39/395,A61K45/00,A61P9/00,A61P15/00,
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DEFINITION AK127751
ACCESSION AK127751
VERSION AK127751.1 GI:34534796
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Ninomiya,K., Wagatsuma,M., Kanda,K., Kondo,H., Yokoi,T.,
Kodaira,H., Furuya,T., Takahashi,M., Kikkawa,E., Omura,Y., Abe,K.,
Kamihara,K., Katsuta,N., Sato,K., Tanikawa,M., Yamazaki,M.,
Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Ota,T., Wakamatsu,A.,
Ishii,S., Yamamoto,J., Isono,Y., Kawai-Hio,Y., Saito,K.,
Nishikawa,T., Kimura,K., Yamashita,H., Matsuo,K., Nakamura,Y.,
Sekine,M., Kikuchi,H., Murakawa,K., Kanehori,K.,
Takahashi-Fujii,A., Oshima,A., Sugiyama,A., Kawakami,B., Suzuki,Y.,
Sugano,S., Nagahari,K., Masuho,Y., Nagai,K. and Isogai,T.
NEDO human cDNA sequencing project
Unpublished
2 (bases 1 to 3566)
Isogai,T. and Yamamoto,J.
Direct Submission
Submitted (15-JUL-2003) Takao Isogai, FLJ Project (HRI Team); 2-6-7
Kazusa-Kamatari, Kisarazu, Chiba 292-0818, Japan
(E-mail:genomics@hri.co.jp, Tel:81-438-52-3975, Fax:81-438-52-3986)
NEDO human cDNA sequencing project supported by Ministry of
Economy, Trade and Industry of Japan; cDNA full insert sequencing:

TITLE
JOURNAL
REFERENCE
AUTHORS
TITLE
JOURNAL

COMMENT

Research Association for Biotechnology (RAB); cDNA library construction: Helix Research Institute (HRI) (supported by Japan Key Technology Center etc.); 5'- & 3'-end one pass sequencing: RAB, HRI, and Biotechnology Center, National Institute of Technology and Evaluation; clone selection for full insert sequencing: HRI and RAB; annotation: HRI and RAB.

FEATURES

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/db_xref="taxon:9606"
/clone="OCBBF2018229"
/tissue_type="brain"
/clone_lib="OCBBF2"
/dev_stage="fetal"
/note="cloning vector: pME18SFL3"
223. .711
/note="unnamed protein product"
/codon_start=1
/protein_id="BAC87114.1"
/db_xref="GI:34534797"
/translation="MIWMSFYAPGLVGINVLRLLTSMYFQCWAVMSSNVPHRVFKA
SRNNFYMGLLLVFLSLLPVAYTIMSLPPSDFCPRCRSVAREHLPRGSLLRG
PRPRIPVLVSCQPVKGHTLGESPMFPRKRVFCQDGNVRSFCVCAVHSSHQPPVAVEC
LK"

CDS

ORIGIN

Query Match 36.4%; Score 428; DB 9; Length 3566;
Best Local Similarity 98.9%; Pred. No. 2.8e-93;
Matches 431; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
QY 1 AACTTCTACATGGCCCTCCTGCTGCTGCTGCTCTTCTCCTCAGCCCTCCTGCGGTGGCCTAC 60
Db |||||
QY 367 AACTTCTACATGGCCCTCCTGCTGCTGCTGCTCTTCTCCTCAGCCCTCCTGCGGTGGCCTAC 426
Db |||||
QY 61 ACCATCATGTCCCTCCACCCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Db |||||
QY 427 ACCATCATGTCCCTCCACCCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 486
Db |||||
QY 121 GCGCGGAGCACCTCCCTCCCGAGGAGCTGCTGCTCAGAGGGCTCGGCCAGAAATCCA 180
Db |||||
QY 487 GCGCGGAGCACCTCCCTCCCGAGGAGCTGCTGCTCAGAGGGCTCGGCCAGAAATCCA 546
Db |||||
QY 181 GTTCTGTTTCATGCCAGCCTGTAAAGGCCATGGAACCTTGGGTGAATCACCAGTGCCA 240
Db |||||
QY 547 GTTCTGTTTCATGCCAGCCTGTAAAGGCCATGGAACCTTGGGTGAATCACCAGTGCCA 606
Db |||||
QY 241 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGTTCGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 300
Db |||||
QY 607 TTTAAGAGGGTTTCTGCCAGGATGGAATGTTAGTTCGTTCTGCTGCTGCTGCTGCTGCTGCTGCT 666
Db |||||
QY 301 TTCAGTAGCCACGACCCCTGTGGCCGTTGAGTGTGCTTGAATGAGGAACTGAGAAATTT 360
Db |||||
QY 667 TTCAGTAGCCACGACCCCTGTGGCCGTTGAGTGTGCTTGAATGAGGAACTGAGAAATTT 726
Db |||||
QY 361 AATTCTCATGTAATTTTCTCAATTAATTAATTTTAACTGATAGTTGTACATATTT 420
Db |||||
QY 727 AATTCTCATGTAATTTTCTCAATTAATTAATTTTAACTGATAGTTGTACATATTT 786
Db |||||
QY 421 GGGGGTACATGTGATA 436
Db |||||
QY 787 GGGGGTTCATACATA 802
Db |||||

RESULT 13
AC084033
LOCUS Homo sapiens 12q BAC RP11-58A17 (Roswell Park Cancer Institute
DEFINITION Human BAC Library) complete sequence.
AC084033
ACCESSION AC084033
VERSION AC084033.33 GI:16572869
KEYWORDS HTG.
SOURCE Homo sapiens (human)

ORGANISM

Homo sapiens

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

REFERENCE

AUTHORS

1 (bases 1 to 162023)

Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chiu,D., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Emerling,S., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Han,J., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., Hernandez,J., Hernandez,O., Hodgson,A., Hogue,M., Holloway,C., Hollins,B., Homs,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Ioshikhes,I., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lee,E., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Marondel,I., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Merscher,S., Metzker,M., Miller,A., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Montgomery,K.T., Morgan,M., Morris,S., Moser,M., Neal,D., Nelson,D., Newton,J., Newton,N., Nguyen,A., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shim,C., Shooshtari,N., Sisson,I., Sodergren,E., Sonaik,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telford,B., Thomas,N., Thomas,S., Usmari,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wall,R., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Kucherlapati,R., Weinstock,G. and Gibbs,R.

Direct Submission
Unpublished
2 (bases 1 to 162023)
Worley,K.C.
Direct Submission
Submitted (11-OCT-2000) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
3 (bases 1 to 162023)
Worley,K.C.
Direct Submission
Submitted (01-NOV-2001) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
4 (bases 1 to 162023)
Worley,K.C.
Direct Submission
Submitted (01-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
5 (bases 1 to 162023)
Worley,K.C.
Direct Submission
Submitted (07-MAR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
6 (bases 1 to 162023)
Worley,K.C.

TITLE

JOURNAL

REFERENCE

AUTHORS

1 (bases 1 to 162023)

TITLE

JOURNAL

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1 (bases 1 to 162023)

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1 (bases 1 to 162023)

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AUTHORS

1 (bases 1 to 162023)

TITLE

TITLE

Direct Submission
Submitted (01-OCT-2002) Human Genome Sequencing Center, Department
of Molecular and Human Genetics, Baylor College of Medicine, One
Baylor Plaza, Houston, TX 77030, USA
On Nov 1, 2001 this sequence version replaced gi:16506862.
INFORMATION: <http://www.hgsc.bcm.tmc.edu/> or email
gc-help@bcm.tmc.edu

COMMENT

CLONE LENGTH: This sequence does not necessarily represent the
entire insert of this clone. Overlapping regions of clones are only
sequenced and submitted once, so the sequence for the remainder of
the insert may be found in the record for the adjacent clones.
Overlapping clones are noted at the beginning and end of the
Features listing.

ANNOTATION OF FEATURES:

STSs are identified using ePCR (Genome Res. 7:541-550) searches
of a local database that includes entries from dbSTS, GDB, and
local mapping efforts.

Repeats are identified using RepeatMasker (A. Smit and P. Green,
unpublished.) for Human and Mouse sequences.

Genes and Region of sequence similarity are identified by BLAST
(Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
EST and cDNA sequences. Genes demonstrate at least two exons
flanked by consensus splice sites that maintained sequence
continuity across the splice junctions. Sequences that are not
identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
standard of double strand coverage with a minimum of 2 clones and 2
reads with no ambiguities or 2 chemistries with a minimum of 2
clones and 3 reads with no ambiguities. If the sequence quality for
a region does not meet this standard, it will be indicated in the
annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
standards - estimated error rate less than 1 per 10,000 bases.
Reports of lowest quality individual bases and measures of base
quality are listed below. Description of the metrics can be found
at URL:
<http://gc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html>.

QUALSTAT-REPORT-----

----- Summary Statistics -----
Contig length: 162023
Phrap values in estimate: 160693
Average error rate (BCM-Phrap estimate): 8.87223e-05
Fraction of Phrap values less than 40 : 0.0163604
Number of consensus changing edits: 145
Number of N's in consensus : 0

Consensus changing edits			Edited+Context	
Position	Original+Context			
54658	caaaagaaga(n)atacaagcag		caaaagaaga(c)atacaagcag	
61881	gcagaaccag(n)tggaatatata		gcagaaccag(t)tggaatatata	
80581	tattaattta(n)ccataaatga		tattaattta(a)ccataaatga	
80667	taatgacccc(n)ctgtgctcag		taatgacccc(a)ctgtgctcag	
111910	tgaagtgcag(n)gatgtgatct		tgaagtgcag(t)gatgtgatct	
121507	ttagggata(n)anncannaat		ttagggata(t)accagtaaat	
121509	tgggtatana(n)ncannaatgg		tgggtatata(c)ccagtaatgg	
121510	gggtatanan(n)cannaatggg		gggtatatat(c)catgaatggg	
121513	tatanannca(n)naatgggatg		tatataccca(g)taatgggatg	
121514	atananncan(n)aatgggatgg		atataccacg(t)aatgggatgg	
121554	tagttctaga(n)ccctgaggaa		tagttctaga(t)ccctgaggaa	
121906	tatacacaca(n)acacatatat		tatatacaca(c)acacatatat	
121940	tatacacaca(g)acacatatat		tatacacaca(c)acacatatat	
121960	tatacacaca(t)acacatatat		tatacacaca(c)acacatatat	
121978	tatacacaca(n)acacatatat		tatacacaca(c)acacatatat	
122027	atatataatg(n)nangaccacc		atatataatg(g)atagaccagc	
122028	tatataatgn(n)angaccaccc		tatataatgg(a)tagaccagcc	

122029 atataatgnn(a)ngaccacccca
122030 tataatgnaa(n)gaccacccag
122036 gnmangacca(c)ccagccagat
122054 gatgataaga(n)atatatatat
128438 ttaaatgttt(n)acaaggcttc
155054 tcgcccaggc(n)ggngngngn
155057 ccaggcngg(n)rgngngngn
155058 ccaggcngn(n)gngngngng
155059 caggcnggn(g)rgngngngn
155060 aggcngngn(n)gngngngnc
155061 ggcngngng(n)rgngngngn
155062 ggcngngng(n)gngngngnc
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155065 gngngngng(n)gngncnncn
155067 ngngngngng(n)gncnncnnc
155069 gngngngng(n)cnncnncn
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155072 ngngngngn(n)cnncnncn
155075 ngngncnnc(n)ncnncnncn
155076 gngncnncn(n)cnncnncn
155077 ngcncnncn(c)cnncnncn
155079 ncnncnnc(n)nnnnnnnn
155080 cncncnnc(n)nnnnnnncn
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155085 ncnncnnc(n)nnnnnnngc
155086 ncnncnnc(n)nnnnnnngt
155087 cncnnnnnn(n)ncnnngctn
155088 cnnnnnnnn(n)cnnnngctnc
155090 nnnnnnnnc(n)nnngctnct
155091 nnnnnnnnc(n)ngctnctnc
155092 nnnnnnnnc(n)ngctnctnc
155093 nnnnnnnnn(n)gctnctnct
155094 nnnnnnnnn(g)ctnctnctn
155097 nncnnngct(n)ctnctnncn
155099 cnnngctnc(c)tnctnncnn
155100 nnnngctncc(t)ctnncnnca
155101 nngctnct(n)ctnnnnncaa
155102 nngctnctn(c)tnnnnncaan
155104 gctnctnct(n)nnnncaann
155105 ctncctnctn(n)nncaannnn
155106 tnctnctn(n)nncaannnt
155107 nctnctnnc(n)ncannnnntn
155108 cctnctnnnn(n)caannntnc
155112 ctnnnnncaa(n)nnntnctct

Query Match 31.5%; Score 370.6; DB 9; Length 162023;
Best Local Similarity 72.8%; Pred. No. 3.7e-79;
Matches 608; Conservative 0; Mismatches 174; Indels 53; Gaps 8;

QY	350	CTGAGAAAATAATTCTCATGTATTTTCTCATTTATTATTATAATTTTAACTGATAGT	409
Db	42553	CTAAGATACTTAATATGATTTTAAATTTTATTTTTAACTATT-ATGAATACATAATAGT	42611
QY	410	TGTACATATTT-GGGGGTACATGTGATATTTGGATACATGTATACAATATATAATGATCA	468
Db	42612	TGTACATATTTACAGAATACACATGATATTTTGATACAAGCATACATGTATAACTGTCA	42671
QY	469	AATCAGGGTAACTGGGATATCCATCACATCAACATTTA-----TTTTTTATT	516
Db	42672	AATCAGAGTAATTGGTATCCATCAACTCAAGCATTTTACCATTCTTTTTTTTTTTT	42731
QY	517	CTTTTTCAGACAGAGTCTCACTCTGTACCCAGGCTGGAGTGGTGGCCATCTCAGCT	576
Db	42732	TTATTCAGATGGAGTTTCATTCTATCACCCAGGCTGGAGTGGTGGCAATCTCAGCT	42791
QY	577	TACTGCAACCTCTGCCTGCCAGGTTCAAGCGATTCTCATGCGCTCCACCTCCCAAGTAGCT	636
Db	42792	CAC TGCAACTTCCATCTCCCGAGGTTCAAGCAATTTCTCTCTGCGCTCCTGAGTAGCT	42851
QY	637	GGGACTACAGGCATGCACCACAATGCCCAACTAAT--TTTTGTATTTTGTAGTAGACGG	694

Db 42852 GGAACACAGGCGATGGGCAACACACCCAGTAAATTATTTGTACTTTTAGTAGACAG 42911
QY 695 GGTTTTGCCATGTTGCCAGGCTGGCCTTGAACCTCCTGGCCTCAACAATCCACTTGCCT 754
Db 42912 GGTTCACCATGTTGCTCAGGCTGGTCTCGAACTCCTGACCTCAAATGATCTGCCACCT 42971
QY 755 CGGCCTCCCAAGTGTATGATTACAGGCGTGAGCCACCGTGCCTGGCCT-AAACATTTA 813
Db 42972 TGGCCTCCCAAGTGTATGAGGATAGAGGTATGAGCCACCATGCCAGCCACAAAGCATTTA 43031
QY 814 TCTTTTCTTTG-----TGTGGGAACCTTTGAAATTATACAAAT 850
Db 43032 TCATTTCTTTGTAGGAACATTCAGTTCTACTCTTTAAGTTATTTTGAATATACAAAT 43091
QY 851 GAATTATTGTTAACTGTCATCTCCCTGCTGTGCTATGGAACACTGGGACTTCTTCCCTCT 910
Db 43092 AAATTATTACTAATCTATCGTTGCCCTACTGTGCTACCAAGCACTACATCTTTTCTCCT 43151
QY 911 ATCTAACTGTATATTGTACCACTTAACCAACCGTACTTCACTCCCACTCCTCTCTATCC 970
Db 43152 ATCCAACCATATTTTATACCCATTAACCTTCTTCTCATCTCC-----CC 43199
QY 971 TTCCCAACCTCTGATCAC-CTCATTCTACTCTCTACCTCCATGAGATCCACTTTTTCAGC 1029
Db 43200 TTCCAGCCTCTAGTAACTATCAATCAACTCTCTACCTCGATGAGATCCACTTTTTCGAGC 43259
QY 1030 TCCACATGTGAGTAAGAAATGCAATATTGTTCTTCTGTCGCTGGCTTATTTACATTA 1089
Db 43260 TCTCACACATGAGCAAGAACATGCAGTATTGTTCTTCTGTCGCTGGATTTTCGCTTA 43319
QY 1090 ACATAATGACTTCCCTGTTCCATCCATGTTGCTGCAAAATGACAGGATTCGTTCTT 1144
Db 43320 ATATAATGCTCTTAAGTTCCATCCATATTTGTTGCAAAATGATAGGATTCATCTT 43374

RESULT 14
AC027633/c
LOCUS AC027633 168283 bp DNA linear HTG 07-JUL-2000
DEFINITION Homo sapiens chromosome 12 clone RP11-489P6, WORKING DRAFT
SEQUENCE, 12 unordered pieces.
AC027633
AC027633.2 GI:7577653
KEYWORDS HTG; HTGS_PHASE1; HTGS_DRAFT.
SOURCE Homo sapiens (human)

ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 168283)
Waterston,R.H.
Unpublished
Waterston,R.H.
Direct Submission
Submitted (30-MAR-2000) Genome Sequencing Center, Washington
University School of Medicine, 4444 Forest Park Parkway, St. Louis,
MO 63108, USA
On Apr 16, 2000 this sequence version replaced gi:7344372.

Center: Washington University Genome Sequencing Center
Center code: WUGSC
Web site: <http://genome.wustl.edu/gsc/index.shtml>
Center project name: H_NH0489P06
Sequencing vector: pBluescript
Chemistry: Dye-primer ET; 100% of reads
Chemistry: Dye-terminator Big Dye; 0% of reads
Assembly program: Phrap; version 0.990319
Consensus quality: 163969 bases at least Q40

Consensus quality: 165146 bases at least Q30
Consensus quality: 165936 bases at least Q20
Insert size: 168000; agarose-fp
Insert size: 167183; sum-of-contigs
Quality coverage: 5.15 in Q20 bases; agarose-fp
Quality coverage: 5.19 in Q20 bases; sum-of-contigs
* NOTE: This is a 'working draft' sequence. It currently
* consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
* arbitrary. Gaps between the contigs are represented as
* runs of N, but the exact sizes of the gaps are unknown.
* This record will be updated with the finished sequence
* as soon as it is available and the accession number will
* be preserved.

1 1384: contig of 1384 bp in length
1385 1484: gap of unknown length
1485 6476: contig of 4992 bp in length
6477 6576: gap of unknown length
6577 11099: contig of 4523 bp in length
11100 11199: gap of unknown length
11200 15458: contig of 4259 bp in length
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22943 23042: gap of unknown length
23043 31175: contig of 8133 bp in length
31176 31275: gap of unknown length
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40328 40427: gap of unknown length
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REFERENCE
AUTHORS
TITLE
JOURNAL
REFERENCE
AUTHORS

Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 162145)
Birren,B., Nusbaum,C. and Lander,E.
Homo sapiens chromosome 11, clone RP11-49619
Unpublished
2 (bases 1 to 162145)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B.,
Camarata,J., Chang,J., Chazaro,B., Choepel,Y., Collymore,A.,
Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S.,
Faro,S., Ferreira,P., FitzGerald,M., Gage,D., Galagan,J.,
Gardyna,S., Gord,S., Graham,L., Grand-Pierre,N., Hagos,B.,
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McCarthy,M., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V.,
Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H.,
O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K.,
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Tsfaye,S., Theodore,J., Topham,K., Travers,M., Vassiliev,H.,
Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Young,G., Zainoun,J.,
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Direct Submission
Submitted (24-AUG-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
3 (bases 1 to 162145)
Birren,B., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S.,
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Direct Submission
Submitted (21-SEP-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
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Zembek,L., Zimmer,A. and Zody,M.
Direct Submission
Submitted (04-OCT-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 4, 2002 this sequence version replaced gi:23266356.
All repeats were identified using RepeatMasker:

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COMMENT

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Submitted (04-OCT-2002) Whitehead Institute/MIT Center for Genome
Research, 320 Charles Street, Cambridge, MA 02141, USA
On Oct 4, 2002 this sequence version replaced gi:23266356.
All repeats were identified using RepeatMasker:

Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
----- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
----- Project Information
Center project name: L28085
Center clone name: 496_I_9

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